



Cura 468 SEQ list 0405.txt  
SEQUENCE LISTING

<110> Edinger, Shlomit R  
Gerlach, Valerie  
MacDougall, John R  
Malyankar, Muriel M  
Smithson, Glennda  
Millet, Isabelle  
Peyman, John A  
Stone, David J  
Gunther, Erik  
Ellerman, Karen  
Shimkets, Richard A  
Padigaru, Muralidhara  
Guo, Xiaojia  
Patturajan, Meera  
Taupier Jr, Raymond J  
Burgess, Catherine E  
Zerhusen, Bryan D  
Kekuda, Ramesh  
Spytek, Kimberly A  
Gangolli, Esha A  
Fernandes, Elma R  
Gorman, Linda

<120> Proteins and Nucleic Acids Encoding Same

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<223> Wherein n is an a or t or c or g.

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                     20                    25                    30  
 Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu  
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 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser  
                     50                    55                    60  
 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu  
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Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp Phe	165	170	175	
His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile	180	185	190	
Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro	195	200	205	
Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn	210	215	220	
Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu	225	230	235	240
Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg	245	250	255	
Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His	260	265	270	
Tyr Lys Trp Lys Pro Tyr Thr Gln Val Glu Xaa Asp Leu Cys Lys Leu	275	280	285	
Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys	290	295	300	
Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile	305	310	315	320
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Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys Ser	340	345	350	
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Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp Gln				
	435	440	445	
Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile Leu				
	450	455	460	
Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp Thr				
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Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser Cys				
	485	490	495	
Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala His				
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Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn Met				
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Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly Arg				
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Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His Lys				
	545	550	555	560
Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys Pro				
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Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr Asp				
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Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu Cys				
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Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His Arg				

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Cys Ile Asp Gly Ile Cys Glu Xaa Gly Cys Asp Asn Val Leu Gly Ser 785 790 795 800																	
Asp Ala Val Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala 805 810 815																	
Cys Thr Ile His Arg Gly Leu Tyr Thr Lys His His His Thr Asn His 820 825 830																	
Tyr His Met Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr 835 840 845																	
Glu Met Asn Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg 850 855 860																	
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Glu Asn Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu  
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Leu Leu Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met  
915 920 925

Pro Arg Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr  
930 935 940

Trp Ala Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg  
945 950 955 960

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<212> DNA

<213> Homo sapiens

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			20					25					30		
Arg	Gly	Asn	Arg	Gly	Ser	Gly	Gln	Leu	Glu	Ala	Ser	Pro	Pro	Arg	Leu
		35					40					45			
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	50					55					60				
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Pro	Glu	Arg	Pro	Ala	Ser	Ser	Ser	Thr	Arg	Gly	Ala	Ala	Gly	Leu	Asp
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Phe	His	Met	Asp	Leu	Arg	Thr	Ser	Ser	Ser	Leu	Val	Ala	Pro	Gly	Phe
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Pro	Pro	Glu	Asp	Phe	Cys	Phe	Tyr	Gln	Gly	Ser	Leu	Arg	Ser	His	Arg
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Leu	Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys	Pro	Arg	Asp	Ser	Val	Asp	Phe
				245					250					255	
Arg	Ala	Ala	Gln	Cys	Ala	Glu	His	Asn	Ser	Arg	Arg	Phe	Arg	Gly	Arg
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Ile	Asp	Gly	Ile	Cys	Glu	Met	Pro	Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe
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			340					345					350		
Leu	Arg	Ser	His	Arg	Asn	Glu	Glu	Leu	Asn	Val	Glu	Thr	Leu	Val	Val
		355					360					365			
Val	Asp	Lys	Lys	Met	Met	Gln	Asn	His	Gly	His	Glu	Asn	Ile	Thr	Thr
	370					375					380				

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Thr	Ile	Gly	Gly	Asn	Ile	Asn	Ile	Ala	Ile	Val	Gly	Leu	Ile	Leu	Leu		405	410	415
Glu	Asp	Glu	Gln	Asp	Ile	Cys	Lys	Ala	Leu	Trp	Cys	His	Arg	Ile	Gly		420	425	430
Arg	Lys	Cys	Glu	Thr	Lys	Phe	Met	Pro	Ala	Ala	Glu	Gly	Thr	Ile	Cys	435	440	445	
Gly	His	Asp	Met	Trp	Cys	Arg	Gly	Gly	Gln	Cys	Val	Lys	Tyr	Gly	Asp	450	455	460	
Glu	Gly	Pro	Lys	Pro	Thr	His	Gly	His	Trp	Ser	Asp	Trp	Ser	Ser	Trp	465	470	475	480
Ser	Pro	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	His	Arg	Ser	Arg		485	490	495
Leu	Cys	Thr	Asn	Pro	Arg	Pro	Ser	His	Gly	Gly	Lys	Phe	Cys	Glu	Gly		500	505	510
Ser	Thr	Arg	Thr	Leu	Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys	Pro	Arg	Asp	515	520	525	
Ser	Val	Asp	Phe	Arg	Ala	Ala	Gln	Cys	Ala	Glu	His	Asn	Ser	Arg	Arg	530	535	540	
Phe	Arg	Gly	Arg	His	Tyr	Lys	Trp	Lys	Pro	Gln	Asp	Leu	Cys	Lys	Leu	545	550	555	560
Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser	Asn	Lys		565	570	575
Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val	Cys	Ile		580	585	590
Asp	Gly	Ile	Cys	Glu	Gly	Cys	Asp	Asn	Val	Leu	Gly	Ser	Asp	Ala	Val	595	600	605	
Glu	Asp	Val	Cys	Gly	Val	Cys	Asn	Gly	Asn	Asn	Ser	Ala	Cys	Thr	Ile	610	615	620	
His	Arg	Gly	Leu	Tyr	Thr	Lys	His	His	His	Thr	Asn	Tyr	Tyr	His	Met	625	630	635	640

Cura 468 SEQ list 0405.txt

Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met Asn  
645 650 655

Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr Tyr  
660 665 670

Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe Ser  
675 680 685

Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn Leu  
690 695 700

Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu Phe  
705 710 715 720

Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg Leu  
725 730 735

Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala Ile  
740 745 750

Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu Pro  
755 760 765

Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr Ala Tyr Ile  
770 775 780

Ala Leu Ala Phe Leu Glu Ser  
785 790

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<211> 2902

<212> DNA

<213> Homo sapiens

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Cura 468 SEQ list 0405.txt

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Cura 468 SEQ list 0405.txt

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<210> 6
<211> 856
<212> PRT
<213> Homo sapiens

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<400> 6
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## Cura 468 SEQ list 0405.txt

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Val Ser His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala	35	40	45
Val Ser Glu Val Glu Pro Ala Phe Leu Gln Val Cys Arg Ala Arg Glu	50	55	60
Leu Arg Leu Cys Val Glu Ala Phe Pro Ile Ala Asn Ser Gln Pro Gly	65	70	75
Phe Leu Asn Leu Ser Asn Val Arg Ser His Trp Arg Glu Gln His Ala	85	90	95
Ser Lys Arg Ile Ile Thr Asn Ala Met Leu Gly Glu Ser Ala Leu Ala	100	105	110
Ser Thr Arg Lys Ser Asn Cys Val Phe Phe Leu Ser Phe Tyr Phe Phe	115	120	125
Gln Ser Gly Met Ile Arg Thr Glu Glu Ala Asp Tyr Phe Leu Arg Pro	130	135	140
Leu Pro Ser His Leu Ser Trp Lys Leu Gly Arg Ala Ala Gln Gly Ser	145	150	155
Ser Pro Ser His Val Leu Tyr Lys Arg Glu Val Leu Val Thr Ser Arg	165	170	175
Thr Trp Glu Leu Ala His Gln Pro Leu His Ser Ser Asp Leu Arg Leu	180	185	190
Gly Leu Pro Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Tyr Met	195	200	205
Pro Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys	210	215	220
Ser Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu	225	230	235
Glu Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln	245	250	255
Asn His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn			

## Cura 468 SEQ list 0405.txt

260		265		270
Met Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn	275	280		285
Ile Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu	290	295		300
Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp	305	310		315
Gln Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile	325		330	335
Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp	340		345	350
Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser	355		360	365
Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala	370		375	380
His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn	385		390	395
Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly	405		410	415
Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His	420		425	430
Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys	435		440	445
Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr	450		455	460
Gly Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu	465		470	475
Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His	485		490	495
Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly	500		505	510
Thr Ile Cys Gly His Glu His Gly Ala Gly Gly Gln Cys Val Lys Tyr				

Cura 468 SEQ list 0405.txt

515		520		525															
Gly	Asp	Glu	Gly	Pro	Lys	Pro	Thr	His	Gly	His	Trp	Ser	Asp	Trp	Ser				
530						535					540								
Ser	Trp	Ser	Pro	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	His	Arg				
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Ser	Arg	Ser	Gln	Asn	Thr	His	Ser	Arg	Pro	Ser	His	Gly	Gly	Lys	Phe				
				565					570					575					
Cys	Glu	Gly	Ser	Thr	Arg	Thr	Leu	Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys				
			580					585					590						
Pro	Arg	Asp	Ser	Val	Asp	Phe	Arg	Ala	Ala	Gln	Cys	Ala	Glu	His	Asn				
		595					600					605							
Ser	Arg	Arg	Phe	Arg	Gly	Arg	His	Tyr	Lys	Trp	Lys	Pro	Asp	Gln	Asp				
		610				615					620								
Leu	Cys	Lys	Leu	Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser				
625					630					635					640				
Leu	Ser	Asn	Lys	Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg				
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Asn	Val	Cys	Ile	Asp	Gly	Ile	Cys	Glu	Arg	Val	Gly	Cys	Asp	Asn	Val				
			660					665					670						
Leu	Gly	Ser	Asp	Ala	Val	Glu	Asp	Val	Cys	Gly	Val	Cys	Asn	Gly	Asn				
		675					680					685							
Asn	Ser	Ala	Cys	Thr	Ile	His	Arg	Gly	Leu	Tyr	Leu	Glu	Tyr	Tyr	His				
		690				695					700								
Met	Val	Thr	Ile	Pro	Ser	Gly	Ala	Arg	Ser	Ile	Arg	Ile	Tyr	Glu	Met				
705					710					715				720					
Asn	Val	Ser	Thr	Ser	Tyr	Ile	Ser	Val	Arg	Asn	Ala	Leu	Arg	Arg	Tyr				
				725					730					735					
Tyr	Leu	Asn	Gly	His	Trp	Thr	Val	Asp	Trp	Pro	Gly	Arg	Tyr	Lys	Phe				
			740					745					750						
Ser	Gly	Thr	Thr	Phe	Asp	Tyr	Arg	Arg	Ser	Tyr	Asn	Glu	Pro	Glu	Asn				
		755					760					765							
Leu	Ile	Ala	Thr	Gly	Pro	Thr	Asn	Glu	Thr	Leu	Ile	Val	Glu	Leu	Leu				

Cura 468 SEQ list 0405.txt

770

775

780

Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg  
785 790 795 800

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805 810 815

Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu  
820 825 830

Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Leu Ala Thr Ala Tyr  
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850 855

<210> 7

<211> 2895

<212> DNA

<213> Homo sapiens

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Cura 468 SEQ list 0405.txt

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Cura 468 SEQ list 0405.txt

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 <211> 952  
 <212> PRT  
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<400> 8

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		35					40					45			
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	50					55					60				
Ala	Gly	Thr	Cys	Val	Arg	His	Gly	Thr	Arg	Ser	Gly	Ser	Ala	Trp	Glu
65					70					75					80

Cura 468 SEQ list 0405.txt

Pro	Glu	Arg	Pro	Ala	Ser	Ser	Ser	Thr	Arg	Gly	Ala	Ala	Gly	Leu	Asp	
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Gly	Lys	Gly	Arg	Asp	Met	Asp	Glu	Ala	Gly	Asn	His	Arg	Ser	Gln	Gln	
			100					105					110			
Thr	Asn	Thr	Gly	Thr	Glu	Asn	Gln	Thr	Leu	His	Val	Leu	Thr	Gln	Tyr	
		115					120					125				
Asp	Leu	Val	Ser	Ala	Tyr	Glu	Val	Asp	His	Arg	Gly	Asp	Tyr	Val	Ser	
	130					135					140					
His	Glu	Ile	Met	His	His	Gln	Arg	Arg	Arg	Arg	Ala	Val	Ala	Val	Ser	
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Glu	Val	Glu	Ser	Leu	His	Leu	Arg	Leu	Lys	Gly	Pro	Arg	His	Asp	Phe	
				165					170					175		
His	Met	Asp	Leu	Arg	Thr	Ser	Ser	Ser	Leu	Val	Ala	Pro	Gly	Phe	Ile	
			180					185					190			
Val	Gln	Thr	Leu	Gly	Lys	Thr	Gly	Thr	Lys	Ser	Val	Gln	Thr	Leu	Pro	
		195					200					205				
Pro	Glu	Asp	Phe	Cys	Phe	Tyr	Gln	Gly	Ser	Leu	Arg	Ser	His	Arg	Asn	
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Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys	Pro	Arg	Asp	Ser	Val	Asp	Phe	Arg	
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Ala	Ala	Gln	Cys	Ala	Glu	His	Asn	Ser	Arg	Arg	Phe	Arg	Gly	Arg	His	
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Tyr	Lys	Trp	Lys	Pro	Tyr	Thr	Gln	Val	Glu	Ala	Asp	Leu	Cys	Lys	Leu	
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Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser	Asn	Lys	
	290					295					300					
Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val	Cys	Ile	
305					310					315					320	
Asp	Gly	Ile	Cys	Glu	Leu	Ser	Val	Val	Ser	Thr	Ser	Ala	His	Met	Pro	
				325					330					335		

Cura 468 SEQ list 0405.txt

Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe	Ile	Leu	Pro	Asp	Glu	Tyr	Lys	Ser	340	345	350
Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	Leu	Arg	Ser	His	Arg	Asn	Glu	Glu	355	360	365
Leu	Asn	Val	Glu	Thr	Leu	Val	Val	Val	Asp	Lys	Lys	Met	Met	Gln	Asn	370	375	380
His	Gly	His	Glu	Asn	Ile	Thr	Thr	Tyr	Val	Leu	Thr	Ile	Leu	Asn	Met	385	390	395
Val	Ser	Ala	Leu	Phe	Lys	Asp	Gly	Leu	Met	Gly	Lys	Asp	Gly	Thr	Arg	405	410	415
His	Asp	His	Ala	Ile	Leu	Leu	Thr	Gly	Leu	Asp	Ile	Cys	Ser	Trp	Lys	420	425	430
Asn	Glu	Pro	Cys	Asp	Thr	Leu	Gly	Phe	Ala	Pro	Ile	Ser	Gly	Met	Cys	435	440	445
Ser	Lys	Tyr	Arg	Ser	Cys	Thr	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Gly	Leu	450	455	460
Ala	Phe	Thr	Ile	Ala	His	Glu	Ser	Gly	His	Asn	Phe	Gly	Met	Ile	His	465	470	475
Asp	Gly	Glu	Gly	Asn	Met	Cys	Lys	Lys	Ser	Glu	Gly	Asn	Ile	Met	Ser	485	490	495
Pro	Thr	Leu	Ala	Gly	Arg	Asn	Gly	Val	Phe	Ser	Trp	Ser	Pro	Cys	Ser	500	505	510
Arg	Gln	Tyr	Leu	His	Lys	Phe	Leu	Ser	Thr	Ala	Gln	Ala	Ile	Cys	Leu	515	520	525
Ala	Asp	Gln	Pro	Lys	Pro	Val	Lys	Glu	Tyr	Lys	Tyr	Pro	Glu	Lys	Leu	530	535	540
Pro	Gly	Glu	Leu	Tyr	Asp	Ala	Asn	Thr	Gln	Cys	Lys	Trp	Gln	Phe	Gly	545	550	555
Glu	Lys	Ala	Lys	Leu	Cys	Met	Leu	Asp	Phe	Lys	Lys	Asp	Ile	Cys	Lys	565	570	575
Ala	Leu	Trp	Cys	His	Arg	Ile	Gly	Arg	Lys	Cys	Glu	Thr	Lys	Phe	Met	580	585	590



Cura 468 SEQ list 0405.txt

Pro	Ala	Ala	Glu	Gly	Thr	Ile	Cys	Gly	His	Asp	Met	Trp	Cys	Arg	Gly	595	600	605
Gly	Gln	Cys	Val	Lys	Tyr	Gly	Asp	Glu	Gly	Pro	Lys	Pro	Thr	His	Gly	610	615	620
His	Trp	Ser	Asp	Trp	Ser	Ser	Trp	Ser	Pro	Cys	Ser	Arg	Thr	Cys	Gly	625	630	635
Gly	Gly	Val	Ser	His	Arg	Ser	Arg	Leu	Cys	Thr	Asn	Pro	Lys	Pro	Ser	645	650	655
His	Gly	Gly	Lys	Phe	Cys	Glu	Gly	Ser	Thr	Arg	Thr	Leu	Lys	Leu	Cys	660	665	670
Asn	Ser	Gln	Lys	Cys	Pro	Arg	Asp	Ser	Val	Asp	Phe	Arg	Ala	Ala	Gln	675	680	685
Cys	Ala	Glu	His	Asn	Ser	Arg	Arg	Phe	Arg	Gly	Arg	His	Tyr	Lys	Trp	690	695	700
Lys	Pro	Tyr	Thr	Gln	Val	Glu	Asp	Gln	Asp	Leu	Cys	Lys	Leu	Tyr	Cys	705	710	715
Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser	Asn	Lys	Val	Lys	725	730	735
Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val	Cys	Ile	Asp	Gly	740	745	750
Ile	Cys	Glu	Arg	Val	Gly	Cys	Asp	Asn	Val	Leu	Gly	Ser	Asp	Ala	Val	755	760	765
Glu	Asp	Val	Cys	Gly	Val	Cys	Asn	Gly	Asn	Asn	Ser	Ala	Cys	Thr	Ile	770	775	780
His	Arg	Gly	Leu	Tyr	Thr	Lys	His	His	His	Thr	Asn	Gln	Tyr	Tyr	His	785	790	795
Met	Val	Thr	Ile	Pro	Ser	Gly	Ala	Arg	Ser	Ile	Arg	Ile	Tyr	Glu	Met	805	810	815
Asn	Val	Ser	Thr	Ser	Tyr	Ile	Ser	Val	Arg	Asn	Ala	Leu	Arg	Arg	Tyr	820	825	830
Tyr	Leu	Asn	Gly	His	Trp	Thr	Val	Asp	Trp	Pro	Gly	Arg	Tyr	Lys	Phe	835	840	845

Cura 468 SEQ list 0405.txt

Ser	Gly	Thr	Thr	Phe	Asp	Tyr	Arg	Arg	Ser	Tyr	Asn	Glu	Pro	Glu	Asn
850						855					860				
Leu	Ile	Ala	Thr	Gly	Pro	Thr	Asn	Glu	Thr	Leu	Ile	Val	Glu	Leu	Leu
865					870					875					880
Phe	Gln	Gly	Arg	Asn	Pro	Gly	Val	Ala	Trp	Glu	Tyr	Ser	Met	Pro	Arg
				885					890					895	
Leu	Gly	Thr	Glu	Lys	Gln	Pro	Pro	Ala	Gln	Pro	Ser	Tyr	Thr	Trp	Ala
			900					905						910	
Ile	Val	Arg	Ser	Glu	Cys	Ser	Val	Ser	Cys	Gly	Gly	Gly	Arg	Cys	Leu
		915					920					925			
Pro	Val	Leu	Leu	Leu	Glu	Ala	Ala	Cys	Gln	Pro	Ser	Ala	Thr	Ala	Tyr
		930				935						940			
Ile	Ala	Leu	Ala	Phe	Leu	Glu	Ser								
945					950										

<210> 9  
 <211> 4488  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
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 ggcacctttg tacagactga caaacctctc tacaccccag ggcagcaagt gtatttccgc 420  
 attgtcacca tggatagcaa cttcgttcca gtgaatgaca agtactccat ggtggaacta 480  
 caggatccaa atagcaacag gattgcacag tggctggaag tggtagctga gcaaggcatt 540  
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Cura 468 SEQ list 0405.txt

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tcaacggtgc aggaatcttt cttagtaaaa atttggtgta ggtacaccta tggaaagccc 780  
atgctagggg cagtgcaggt atctgtgtgt cagaaggcaa atacttactg gtatcgagag 840  
gtggaacggg aacagcttcc tgacaaatgc aggaacctct ctggacagac tgacaaaaca 900  
ggatgtttct cagcacctgt ggacatggcc acctttgacc tcattggata tgcgtacagc 960  
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ttttaccatc caaatctccc cttcagtggg aagatgctgc tcaagtttcc gcaaggcggg 1140  
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ggcccatggg actttcctca gcccctcatt gacccaatgc cccaagggca ttcgagccag 1980  
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Cura 468 SEQ list 0405.txt

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 agatctccag aatacagcac tgctatgggt ggcggtgggtc atccagaggc ttttgagtca 2160  
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Cura 468 SEQ list 0405.txt

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<210> 10

<211> 1492

<212> PRT

<213> Homo sapiens

<400> 10

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Ala	Glu	Glu	Leu	Pro	Asn	Tyr	Leu	Val	Thr	Leu	Pro	Ala	Arg	Leu	Asn
			20					25					30		

## Cura 468 SEQ list 0405.txt

Phe	Pro	Ser 35	Val	Gln	Lys	Val	Cys 40	Leu	Asp	Leu	Ser	Pro 45	Gly	Tyr	Ser
Asp	Val 50	Lys	Phe	Thr	Val	Thr 55	Leu	Glu	Thr	Lys	Asp 60	Lys	Thr	Gln	Lys
Leu 65	Leu	Glu	Tyr	Ser	Gly 70	Leu	Lys	Lys	Arg	His 75	Leu	His	Cys	Ile	Ser 80
Phe	Leu	Val	Pro	Pro 85	Pro	Ala	Gly	Gly	Thr 90	Glu	Glu	Val	Ala	Thr 95	Ile
Arg	Val	Ser	Gly 100	Val	Gly	Asn	Asn	Ile 105	Ser	Phe	Glu	Glu	Lys 110	Lys	Lys
Val	Leu	Ile 115	Gln	Arg	Gln	Gly	Asn 120	Gly	Thr	Phe	Val	Gln 125	Thr	Asp	Lys
Pro	Leu 130	Tyr	Thr	Pro	Gly	Gln 135	Gln	Val	Tyr	Phe	Arg 140	Ile	Val	Thr	Met
Asp 145	Ser	Asn	Phe	Val	Pro 150	Val	Asn	Asp	Lys	Tyr 155	Ser	Met	Val	Glu	Leu 160
Gln	Asp	Pro	Asn 165	Ser	Asn	Arg	Ile	Ala	Gln 170	Trp	Leu	Glu	Val	Val 175	Pro
Glu	Gln	Gly	Ile 180	Val	Asp	Leu	Ser	Phe 185	Gln	Leu	Ala	Pro	Glu 190	Ala	Met
Leu	Gly	Thr 195	Tyr	Thr	Val	Ala	Val 200	Ala	Glu	Gly	Lys	Thr 205	Phe	Gly	Thr
Phe	Ser 210	Val	Glu	Glu	Tyr	Val 215	Leu	Ser	Pro	Phe	Leu 220	Leu	Leu	Leu	Ser
Ser 225	Val	Leu	Pro	Lys	Phe 230	Lys	Val	Glu	Val	Val 235	Glu	Pro	Lys	Glu	Leu 240
Ser	Thr	Val	Gln 245	Glu	Ser	Phe	Leu	Val	Lys 250	Ile	Cys	Cys	Arg	Tyr 255	Thr
Tyr	Gly	Lys	Pro 260	Met	Leu	Gly	Ala	Val 265	Gln	Val	Ser	Val	Cys 270	Gln	Lys
Ala	Asn	Thr 275	Tyr	Trp	Tyr	Arg	Glu 280	Val	Glu	Arg	Glu	Gln 285	Leu	Pro	Asp

Cura 468 SEQ list 0405.txt

Lys	Cys	Arg	Asn	Leu	Ser	Gly	Gln	Thr	Asp	Lys	Thr	Gly	Cys	Phe	Ser
290						295					300				
Ala	Pro	Val	Asp	Met	Ala	Thr	Phe	Asp	Leu	Ile	Gly	Tyr	Ala	Tyr	Ser
305					310					315					320
His	Gln	Ile	Asn	Ile	Val	Ala	Thr	Val	Val	Glu	Glu	Gly	Thr	Gly	Val
				325					330					335	
Glu	Ala	Asn	Ala	Thr	Gln	Asn	Ile	Tyr	Ile	Ser	Pro	Gln	Met	Gly	Ser
			340					345					350		
Met	Thr	Phe	Glu	Asp	Thr	Ser	Asn	Phe	Tyr	His	Pro	Asn	Phe	Pro	Phe
		355					360					365			
Ser	Gly	Lys	Met	Leu	Leu	Lys	Phe	Pro	Gln	Gly	Gly	Val	Leu	Pro	Cys
	370					375					380				
Lys	Asn	His	Leu	Val	Phe	Leu	Val	Ile	Tyr	Gly	Thr	Asn	Gly	Thr	Phe
385					390					395					400
Asn	Gln	Thr	Leu	Val	Thr	Asp	Asn	Asn	Gly	Leu	Ala	Pro	Phe	Thr	Leu
				405					410					415	
Glu	Thr	Ser	Gly	Trp	Asn	Gly	Thr	Asp	Val	Ser	Leu	Glu	Gly	Lys	Phe
			420					425					430		
Gln	Met	Glu	Asp	Leu	Val	Tyr	Asn	Pro	Glu	Gln	Val	Pro	Arg	Tyr	Tyr
		435					440					445			
Gln	Asn	Ala	Tyr	Leu	His	Leu	Arg	Pro	Phe	Tyr	Ser	Thr	Thr	Arg	Ser
						455					460				
Phe	Leu	Gly	Ile	His	Arg	Leu	Asn	Gly	Pro	Leu	Lys	Cys	Gly	Gln	Pro
465					470					475					480
Gln	Glu	Val	Leu	Val	Asp	Tyr	Tyr	Ile	Asp	Pro	Ala	Asp	Ala	Ser	Pro
				485					490					495	
Asp	Gln	Glu	Ile	Ser	Phe	Ser	Tyr	Tyr	Leu	Ile	Gly	Lys	Gly	Ser	Leu
			500					505					510		
Val	Met	Glu	Gly	Gln	Lys	His	Leu	Asn	Ser	Lys	Lys	Lys	Gly	Leu	Lys
		515					520					525			
Ala	Ser	Phe	Ser	Leu	Ser	Leu	Thr	Phe	Thr	Ser	Arg	Leu	Ala	Pro	Asp
						535					540				

Cura 468 SEQ list 0405.txt

Pro	Ser	Leu	Val	Ile	Tyr	Ala	Ile	Phe	Pro	Ser	Gly	Gly	Val	Val	Ala
545					550					555					560
Asp	Lys	Ile	Gln	Phe	Ser	Val	Glu	Met	Cys	Phe	Asp	Asn	Gln	Gln	Leu
				565					570					575	
Pro	Gly	Ala	Glu	Val	Glu	Leu	Gln	Leu	Gln	Ala	Ala	Pro	Gly	Ser	Leu
			580					585					590		
Cys	Ala	Leu	Arg	Ala	Val	Asp	Glu	Ser	Val	Leu	Leu	Leu	Arg	Pro	Asp
		595					600					605			
Arg	Glu	Leu	Ser	Asn	Arg	Ser	Val	Tyr	Gly	Met	Phe	Pro	Phe	Trp	Tyr
	610					615					620				
Gly	His	Tyr	Pro	Tyr	Gln	Val	Ala	Glu	Tyr	Asp	Gln	Cys	Pro	Val	Ser
625					630					635					640
Gly	Pro	Trp	Asp	Phe	Pro	Gln	Pro	Leu	Ile	Asp	Pro	Met	Pro	Gln	Gly
				645					650					655	
His	Ser	Ser	Gln	Arg	Ser	Ile	Ile	Trp	Arg	Pro	Ser	Phe	Ser	Glu	Gly
			660					665					670		
Thr	Asp	Leu	Phe	Ser	Phe	Phe	Arg	Asp	Val	Gly	Leu	Lys	Ile	Leu	Ser
		675					680					685			
Asn	Ala	Lys	Ile	Lys	Lys	Pro	Val	Asp	Cys	Ser	His	Arg	Ser	Pro	Glu
	690					695					700				
Tyr	Ser	Thr	Ala	Met	Gly	Gly	Gly	Gly	His	Pro	Glu	Ala	Phe	Glu	Ser
705					710					715					720
Ser	Thr	Pro	Leu	His	Gln	Ala	Glu	Asp	Ser	Gln	Val	Arg	Gln	Tyr	Phe
				725					730					735	
Pro	Glu	Thr	Trp	Leu	Trp	Asp	Leu	Phe	Pro	Ile	Gly	Asn	Ser	Gly	Lys
			740					745					750		
Glu	Ala	Val	His	Val	Thr	Val	Pro	Asp	Ala	Ile	Thr	Glu	Trp	Lys	Ala
		755					760					765			
Met	Ser	Phe	Cys	Thr	Ser	Gln	Ser	Arg	Gly	Phe	Gly	Leu	Ser	Pro	Thr
	770					775					780				
Val	Gly	Leu	Thr	Ala	Phe	Lys	Pro	Phe	Phe	Val	Asp	Leu	Thr	Leu	Pro
785					790					795					800



Cura 468 SEQ list 0405.txt

Tyr	Ser	Val	Val	Arg	Gly	Glu	Ser	Phe	Arg	Leu	Thr	Ala	Thr	Ile	Phe	
				805					810					815		
Asn	Tyr	Leu	Lys	Asp	Cys	Ile	Arg	Val	Gln	Thr	Asp	Leu	Ala	Lys	Ser	
			820					825					830			
His	Glu	Tyr	Gln	Leu	Glu	Ser	Trp	Ala	Asp	Ser	Gln	Thr	Ser	Ser	Cys	
		835					840					845				
Leu	Cys	Ala	Asp	Asp	Ala	Lys	Thr	His	His	Trp	Asn	Ile	Thr	Ala	Val	
	850					855					860					
Lys	Leu	Gly	His	Ile	Asn	Phe	Thr	Ile	Ser	Thr	Lys	Ile	Leu	Asp	Ser	
865					870					875					880	
Asn	Glu	Pro	Cys	Gly	Gly	Gln	Lys	Gly	Phe	Val	Pro	Gln	Lys	Gly	Arg	
				885					890					895		
Ser	Asp	Thr	Leu	Ile	Lys	Pro	Val	Leu	Val	Lys	Pro	Glu	Gly	Val	Leu	
			900					905					910			
Val	Glu	Lys	Thr	His	Ser	Ser	Leu	Leu	Cys	Pro	Lys	Gly	Gly	Lys	Val	
		915					920					925				
Ala	Ser	Glu	Ser	Val	Ser	Leu	Glu	Leu	Pro	Val	Asp	Ile	Val	Pro	Asp	
		930				935					940					
Ser	Thr	Lys	Ala	Tyr	Val	Thr	Val	Leu	Gly	Asp	Ile	Met	Gly	Thr	Ala	
945					950					955					960	
Leu	Gln	Asn	Leu	Asp	Gly	Leu	Val	Gln	Met	Pro	Ser	Gly	Cys	Gly	Glu	
				965					970					975		
Gln	Asn	Met	Val	Leu	Phe	Ala	Pro	Ile	Ile	Tyr	Val	Leu	Gln	Tyr	Leu	
			980					985					990			
Glu	Lys	Ala	Gly	Leu	Leu	Thr	Glu	Glu	Ile	Arg	Ser	Arg	Ala	Val	Gly	
		995					1000					1005				
Phe	Leu	Glu	Ile	Gly	Tyr	Gln	Lys	Glu	Leu	Met	Tyr	Lys	His	Ser	Asn	
	1010					1015					1020					
Gly	Ser	Tyr	Ser	Ala	Phe	Gly	Glu	Arg	Asp	Gly	Asn	Gly	Asn	Thr	Trp	
1025				1030					1035						1040	
Leu	Thr	Ala	Phe	Val	Thr	Lys	Cys	Phe	Gly	Gln	Ala	Gln	Lys	Phe	Ile	
			1045						1050					1055		

Cura 468 SEQ list 0405.txt

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 Asn Gln Leu Pro Ser Gly Cys Tyr Ala Asn Val Gly Asn Leu Leu His  
 1075 1080 1085  
 Thr Ala Met Lys Gly Gly Val Asp Asp Glu Val Ser Leu Thr Ala Tyr  
 1090 1095 1100  
 Val Thr Ala Ala Leu Leu Glu Met Gly Lys Asp Val Asp Asp Pro Met  
 1105 1110 1115 1120  
 Val Ser Gln Gly Leu Arg Cys Leu Lys Asn Ser Ala Thr Ser Thr Thr  
 1125 1130 1135  
 Asn Leu Tyr Thr Gln Ala Leu Leu Ala Tyr Ile Phe Ser Leu Ala Gly  
 1140 1145 1150  
 Glu Met Asp Ile Arg Asn Ile Leu Leu Lys Gln Leu Asp Gln Gln Ala  
 1155 1160 1165  
 Ile Ile Ser Gly Glu Ser Ile Tyr Trp Ser Gln Lys Pro Thr Pro Ser  
 1170 1175 1180  
 Ser Asn Ala Ser Pro Trp Ser Glu Pro Ala Ala Val Asp Val Glu Leu  
 1185 1190 1195 1200  
 Thr Ala Tyr Ala Leu Leu Ala Gln Leu Thr Lys Pro Ser Leu Thr Gln  
 1205 1210 1215  
 Lys Glu Ile Ala Lys Ala Thr Ser Ile Val Ala Trp Leu Ala Lys Gln  
 1220 1225 1230  
 His Asn Ala Tyr Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala  
 1235 1240 1245  
 Leu Gln Ala Leu Ala Lys Tyr Ala Thr Thr Ala Tyr Met Pro Ser Glu  
 1250 1255 1260  
 Glu Ile Asn Leu Val Val Lys Ser Thr Glu Asn Phe Gln Arg Thr Phe  
 1265 1270 1275 1280  
 Asn Ile Gln Ser Val Asn Arg Leu Val Phe Gln Gln Asp Thr Leu Pro  
 1285 1290 1295  
 Asn Val Pro Gly Met Tyr Thr Leu Glu Ala Ser Gly Gln Gly Cys Val  
 1300 1305 1310

Cura 468 SEQ list 0405.txt

Tyr Val Gln Thr Val Leu Arg Tyr Asn Ile Leu Pro Pro Thr Asn Met  
 1315 1320 1325

Lys Thr Phe Ser Leu Ser Val Glu Ile Gly Lys Ala Arg Cys Glu Gln  
 1330 1335 1340

Pro Thr Ser Pro Arg Ser Leu Thr Leu Thr Ile His Thr Ser Tyr Val  
 1345 1350 1355 1360

Gly Ser Arg Ser Ser Ser Asn Met Ala Ile Val Glu Val Lys Met Leu  
 1365 1370 1375

Ser Gly Phe Ser Pro Met Glu Gly Thr Asn Gln Leu Leu Leu Gln Gln  
 1380 1385 1390

Pro Leu Val Lys Lys Val Glu Phe Gly Thr Asp Thr Leu Asn Ile Tyr  
 1395 1400 1405

Leu Asp Glu Leu Ile Lys Asn Thr Gln Thr Tyr Thr Phe Thr Ile Ser  
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Gln Ser Val Leu Val Thr Asn Leu Lys Pro Ala Thr Ile Lys Val Tyr  
 1425 1430 1435 1440

Asp Tyr Tyr Leu Pro Gly Ser Phe Lys Leu Ser Gln Tyr Thr Ile Val  
 1445 1450 1455

Trp Ser Met Asn Asn Asp Ser Ile Val Asp Ser Val Ala Arg His Pro  
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Glu Pro Pro Pro Phe Lys Thr Glu Ala Phe Ile Pro Ser Leu Pro Gly  
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Ser Val Asn Asn  
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 <213> Homo sapiens

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Cura 468 SEQ list 0405.txt

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<211> 326

<212> PRT

<213> Homo sapiens

<400> 12

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			20					25					30		

Val	Phe	Thr	Val	Val	Ser	Thr	Ile	Met	Met	Gly	Leu	Leu	Met	Phe	Ser
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## Cura 468 SEQ list 0405.txt

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Leu	Ile	Asp	Gly	Phe	Leu	Ile	Val	Glu	Glu	Arg	Thr	Glu	Asp	Thr	Asp		
	290					295					300						
Cys	Asp	Gly	Ser	Pro	Leu	Pro	Glu	Tyr	Phe	Thr	Glu	Val	Thr	Ile	Ile		

305

310

315

320

Pro Lys Gln Pro Arg Ile  
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&lt;211&gt; 850

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

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&lt;210&gt; 14

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

Cura 468 SEQ list 0405.txt

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Gly	His	Arg	Ala	Val	Val	Phe	Asp	Arg	Phe	Arg	Gly	Val	Gln	Asp	Ile	35	40	45	
Val	Val	Gly	Lys	Gly	Thr	His	Cys	Leu	Ile	Pro	Trp	Leu	Gln	Lys	Ser	50	55	60	
Ile	Ile	Phe	Asp	Cys	Arg	Ser	Gln	Pro	Arg	Asn	Val	Pro	Val	Ile	Thr	65	70	75	80
Gly	Ser	Lys	Asp	Leu	Gln	Asn	Val	Asn	Leu	Thr	Leu	Arg	Ile	Ile	Phe	85	90	95	
Arg	Pro	Val	Ala	Ser	Gln	Leu	Pro	His	Ile	Phe	Thr	Ser	Ser	Gly	Glu	100	105	110	
Asp	His	Asp	Glu	Arg	Val	Pro	Pro	Ser	Ile	Thr	Asn	Lys	Ile	Leu	Lys	115	120	125	
Ser	Val	Val	Ala	Arg	Phe	Glu	Ala	Gly	Glu	Leu	Ile	Thr	Gln	Arg	Glu	130	135	140	
Gln	Ile	Ser	Arg	Gln	Val	Ser	Asp	Asp	Leu	Thr	Glu	Pro	Ala	Ala	Thr	145	150	155	160
Phe	Gly	Leu	Ile	Leu	Asp	Asp	Val	Ser	Leu	Thr	Tyr	Leu	Thr	Phe	Gly	165	170	175	
Lys	Glu	Phe	Ile	Glu	Ala	Val	Glu	Ala	Lys	Gln	Ile	Ala	Gln	Gln	Glu	180	185	190	
Ala	Glu	Arg	Ala	Arg	Phe	Val	Val	Glu	Lys	Ala	Glu	Gln	Gln	Lys	Lys	195	200	205	
Ala	Ala	Ile	Ile	Ser	Ala	Glu	Gly	Asp	Ser	Lys	Val	Ala	Glu	Leu	Ile	210	215	220	
Thr	Asn	Ser	Leu	Ala	Thr	Ala	Gly	Asp	Ala	Leu	Ile	Glu	Leu	Arg	Lys	225	230	235	240
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<211> 2011

<212> DNA

<213> Homo sapiens

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Cura 468 SEQ list 0405.txt

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<211> 666

<212> PRT

<213> Homo sapiens

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			20					25					30		

## Cura 468 SEQ list 0405.txt

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65					70					75					80
Leu	Pro	Trp	Thr	Gln	His	Ser	Pro	His	Thr	Arg	Leu	Arg	Arg	Ser	Gly
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Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met
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Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly
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Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr
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145					150					155					160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val
				165					170					175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val
			180					185					190		
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser
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225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
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Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly
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Cura 468 SEQ list 0405.txt

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Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	
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Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	
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Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	
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Thr	Ala	Thr	Thr	Ala	Gln	Gly	Ser	Ser	Thr	Ala	Ala	Arg	Ser	Ala	Arg	
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Pro	Ala	Arg	Val	Ser	Ser	Ala	Ser	Ala	Gly	Pro	Leu	Arg	Arg	Arg	Thr	
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Cura 468 SEQ list 0405.txt

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Leu Asn Val Ala Leu Leu Asn Val Ile Ser Asn Gln Glu Cys Asn Ile  
595 600 605

Lys His Arg Gly Arg Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr  
610 615 620

His Asn Cys Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys  
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<211> 634

<212> DNA

<213> Homo sapiens

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Cura 468 SEQ list 0405.txt

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 Arg Lys Met Asp Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp  
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 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Gln Phe  
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 Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Thr Arg Lys Leu Lys Asp  
                     100                    105                    110  
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<400> 19

Cura 468 SEQ list 0405.txt

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<210> 20  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
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 20 25 30  
 Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln  
 35 40 45  
 Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys  
 50 55 60

Cura 468 SEQ list 0405.txt

Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
65					70					75					80
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				85					90					95	
Tyr	Arg	Glu	Glu	Arg	Glu	Arg	Lys	His	His	Leu	Lys	His	Gly	Pro	Asn
			100					105					110		
Ala	Pro	Ser	Leu	Tyr	Asp	Asn	Leu	Ser	Lys	Lys	Arg	Gly	Gly	Leu	Trp
		115					120					125			
Trp	Thr	Tyr	Leu	Leu	Ser	Leu	Ile	Phe	Lys	Ala	Ala	Val	Asp	Ala	Gly
	130					135					140				
Phe	Leu	Tyr	Ile	Phe	His	Arg	Leu	Tyr	Lys	Asp	Tyr	Asp	Met	Pro	Arg
145					150					155					160
Val	Val	Ala	Cys	Ser	Val	Glu	Pro	Cys	Pro	His	Thr	Val	Asp	Cys	Tyr
				165					170					175	
Ile	Ser	Arg	Pro	Thr	Glu	Lys	Lys	Val	Phe	Thr	Tyr	Phe	Met	Val	Thr
			180					185					190		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Phe	Tyr	Leu
		195					200					205			
Val	Gly	Lys	Arg	Cys	Met	Glu	Ile	Phe	Gly	Pro	Arg	His	Arg	Arg	Pro
	210					215					220				
Arg	Cys	Arg	Glu	Cys	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Leu	Ser
225					230					235					240
Gln	Gly	Gly	His	Pro	Glu	Asp	Gly	Asn	Ser	Val	Leu	Met	Lys	Ala	Gly
				245				250						255	
Ser	Ala	Pro	Val	Asp	Ala	Gly	Gly	Tyr	Pro						
			260					265							

<210> 21

<211> 546

<212> DNA

<213> Homo sapiens

<400> 21

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Cura 468 SEQ list 0405.txt

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 tgtgaactaa atccacagcc acataataat caaaacagaa aagcaaaaga aagccacttc 180  
 aggaaatacc acggtcacac ctcagttggc ttcattgctac agattataga aaatatgttg 240  
 ctgccccgggc caccaatctg ttggttcaca ttactacgtg agcaatgtaa gtgtttgcaa 300  
 gaagccatcc actatctaaa tatcagatat agatgctcca aagcagctac gtcagtgatg 360  
 agaacagaga aaatacgtag caacatttca ttaagttgaa ttctaatact taaaaggctc 420  
 ctttttagtac tgacattctg gatttttaaaa gttatgttga ccgcatgttc tcactcacia 480  
 gtgggagttg aacaatgaga acacacggac acggggaagg gaacatcaca caccagggcc 540  
 tgtcag 546

<210> 22  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
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 Trp Phe Thr Leu Leu Arg Glu Gln Cys Lys Cys Leu Gln Glu Ala Ile  
                     20                    25                    30  
 His Tyr Leu Asn Ile Arg Tyr Arg Cys Ser Lys Ala Ala Thr Ser Val  
             35                    40                    45  
 Met Arg Thr Glu Lys Ile Arg Ser Asn Ile Ser Leu Ser  
         50                    55                    60

<210> 23  
 <211> 2309  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (2196)  
 <223> Wherein n is an a o t t o r c o r g.



Cura 468 SEQ list 0405.txt

<400> 23

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acaagcatac acaatgggga attgacttct tggaaagata tgccaaattt gttaaagaga 180
ggatagaaat tgaacagAAC tatgcgaaac aattgagaaa tctgggttaag aagtactgcc 240
ccaaacgttc atccaaagat gaagagccac ggtttacctc gtgtgtagcc ttttttaata 300
tccttaatga gttaaatac tatgcaggac agcgagaagt ttagcagaa gaaatggcgc 360
acagagtgtA tgggtgaatta atgagatatg ctcatgatct gaaaactgaa agaaaaatgc 420
atctgcaaga aggacgaaaa gctcaacaat atcttgacat gtgctggaaa cagatgggta 480
atagtaaaaa gaagtttgaa agagaatgtA gagaggcaga aaaggcacia cagagttatg 540
aaagattgga taatgatact aatgcaacca aggagatgt tgaaaatgcc aaacagcagt 600
tgaatctgcg tacgcatatg gccgatgaaa ataaaaatgc atatgctgca caattacaaa 660
actttaatgg agaacaacat aaacattttt atgtagtgtA tcctcagatt tacaagcaac 720
tacaagaaat ggacgaacga aggactatta aactcagtga gtgttacaga ggatttgctg 780
actcagaacg caaagttatt cccatcattt caaaatgttt ggaaggaatg attcttgag 840
caaaatcagt tgatgaaaga agagactctc aaatgggtgg agactccttc aaatctgggt 900
ttgaacctcc aggagacttt ccatttgaag attacagtca acatatatat agaaccattt 960
ctgatgggac tatcagtgca tccaaacagg agagtgggaa gatggatgcc aaaaccccag 1020
taggaaaggc caagggcaaa ttgtggctct ttggaaagaa gccaaagggc ccagcactag 1080
aagatttcag tcatctgcca ccagaacaga gacgtaaaaa actacagcag cgcattgatg 1140
aacttaacag agaactacag aaagaatcag accaaaaaga tgcactcaac aaaatgaaag 1200
atgtatatga gaaggatcca caaatggggg atccaggagg tttgcagcct aaattagcag 1260
agaccatgaa taacattgac cgctacgaa tggaaatcca taagaatgag gcttggctct 1320
ctgaagtcga aggcaaaaca ggtgggagag gagacagaag acatagcagt gacataaatc 1380

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Cura 468 SEQ list 0405.txt

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aagtcctggtg gccaccccag cagcatgggtc accacaatga gtttgatgat gaatttgagg 1500  
atgatgatcc cttgcctgct attggacact gcaaagctat ctaccctttt gatggacata 1560  
atgaaggtac tctagcaatg aaagaagggtg aagttctcta cattatagag gaggacaaag 1620  
gtgacggatg gacaagagct cggagacaga acggtgaaga aggctacgtt cccacgtcat 1680  
acatagatgt aactctagag aaaaacagta aaggttcctg aagaggggtt ctgaggaaat 1740  
gggcaagatg ttgaaggagg ttacatgcag ctgcttttgg gggaggggtat tagagttgtc 1800  
aggctcaaag agagtgagag aagcaagttg catgagtgc tgcagacatg attttttttt 1860  
tactaacttc attagcattt ccatacattg tttttaaaaa tcataatacc aacccttaag 1920  
ttcctagttc acagttattc ccacaaaaga aaaagccaac aatagtgtac catttttcta 1980  
ttttatttta ttgctgtcta atcaataaag aatgcagagc tgtcaaaaaa tgtgtcttac 2040  
atthagctgt cccaacagga ttgtcttccc tcccagctct gggttttaatt ggcttttaga 2100  
cccactatct gtcagatcct tgccatctgt cagtgtctgc ctgcgccacc tccgtgcttg 2160  
cctaacatcc tgttgcatgt ctagcgtgat tgagcnagat tttcaggcat gtcttttagaa 2220  
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<210> 24

<211> 547

<212> PRT

<213> Homo sapiens

<400> 24

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His Thr Gln Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val  
20 25 30

Lys Glu Arg Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn  
35 40 45

Cura 468 SEQ list 0405.txt

Leu	Val	Lys	Lys	Tyr	Cys	Pro	Lys	Arg	Ser	Ser	Lys	Asp	Glu	Glu	Pro	50	55	60	
Arg	Phe	Thr	Ser	Cys	Val	Ala	Phe	Phe	Asn	Ile	Leu	Asn	Glu	Leu	Asn	65	70	75	80
Asp	Tyr	Ala	Gly	Gln	Arg	Glu	Val	Val	Ala	Glu	Glu	Met	Ala	His	Arg	85	90	95	
Val	Tyr	Gly	Glu	Leu	Met	Arg	Tyr	Ala	His	Asp	Leu	Lys	Thr	Glu	Arg	100	105	110	
Lys	Met	His	Leu	Gln	Glu	Gly	Arg	Lys	Ala	Gln	Gln	Tyr	Leu	Asp	Met	115	120	125	
Cys	Trp	Lys	Gln	Met	Gly	Asn	Ser	Lys	Lys	Lys	Phe	Glu	Arg	Glu	Cys	130	135	140	
Arg	Glu	Ala	Glu	Lys	Ala	Gln	Gln	Ser	Tyr	Glu	Arg	Leu	Asp	Asn	Asp	145	150	155	160
Thr	Asn	Ala	Thr	Lys	Ala	Asp	Val	Glu	Asn	Ala	Lys	Gln	Gln	Leu	Asn	165	170	175	
Leu	Arg	Thr	His	Met	Ala	Asp	Glu	Asn	Lys	Asn	Ala	Tyr	Ala	Ala	Gln	180	185	190	
Leu	Gln	Asn	Phe	Asn	Gly	Glu	Gln	His	Lys	His	Phe	Tyr	Val	Val	Ile	195	200	205	
Pro	Gln	Ile	Tyr	Lys	Gln	Leu	Gln	Glu	Met	Asp	Glu	Arg	Arg	Thr	Ile	210	215	220	
Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe	Ala	Asp	Ser	Glu	Arg	Lys	Val	225	230	235	240
Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu	Gly	Met	Ile	Leu	Ala	Ala	Lys	245	250	255	
Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln	Met	Val	Val	Asp	Ser	Phe	Lys	260	265	270	
Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe	Pro	Phe	Glu	Asp	Tyr	Ser	Gln	275	280	285	
His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly	Thr	Ile	Ser	Ala	Ser	Lys	Gln	290	295	300	

Cura 468 SEQ list 0405.txt

Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr	Pro	Val	Gly	Lys	Ala	Lys	Gly	305	310	315									320
Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro	Lys	Gly	Pro	Ala	Leu	Glu	Asp		325	330								335	
Phe	Ser	His	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg		340	345							350		
Ile	Asp	Glu	Leu	Asn	Arg	Glu	Leu	Gln	Lys	Glu	Ser	Asp	Gln	Lys	Asp	355		360					365				
Ala	Leu	Asn	Lys	Met	Lys	Asp	Val	Tyr	Glu	Lys	Asp	Pro	Gln	Met	Gly	370		375					380				
Asp	Pro	Gly	Ser	Leu	Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	385	390	395								400	
Asp	Arg	Leu	Arg	Met	Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu		405	410							415		
Val	Glu	Gly	Lys	Thr	Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp		420	425					430				
Ile	Asn	His	Leu	Val	Thr	Gln	Gly	Arg	Glu	Ser	Pro	Glu	Gly	Ser	Tyr	435		440					445				
Thr	Asp	Asp	Ala	Asn	Gln	Glu	Val	Arg	Gly	Pro	Pro	Gln	Gln	His	Gly	450	455	460									
His	His	Asn	Glu	Phe	Asp	Asp	Glu	Phe	Glu	Asp	Asp	Asp	Pro	Leu	Pro	465	470	475								480	
Ala	Ile	Gly	His	Cys	Lys	Ala	Ile	Tyr	Pro	Phe	Asp	Gly	His	Asn	Glu		485	490							495		
Gly	Thr	Leu	Ala	Met	Lys	Glu	Gly	Glu	Val	Leu	Tyr	Ile	Ile	Glu	Glu		500	505					510				
Asp	Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ala	Arg	Arg	Gln	Asn	Gly	Glu	Glu	515		520					525				
Gly	Tyr	Val	Pro	Thr	Ser	Tyr	Ile	Asp	Val	Thr	Leu	Glu	Lys	Asn	Ser	530	535	540									
Lys	Gly	Ser														545											

Cura 468 SEQ list 0405.txt

<210> 25  
 <211> 1787  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
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 ggatcttcag agcagagcct ggagaccagc agcatcccat ttctcaggcg gtgtgctggc 180  
 gttccatgcg acgtggctgt gcagtgctgg gagccctggg gctgctggcc ggtgcagggtg 240  
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 cgcaagtgag ggatcagcca cgctggctcc tggctctgcca tgagggctgg agccccgccc 480  
 tggggctgca gatctgctgg agccttgggc atctcagact cactcaccac aaggaggtaa 540  
 acctcactga catcaaactc aacagttccc aggagtctgc tcagctctct cctagactgg 600  
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 gcacttctgg tcaagttggt tccctcagat gctctgagtg tggagcgagg cccttggtt 720  
 cccggatagt tgggtgggcag tctgtggctc ctgggcgctg gccgtggcag gccagcgtgg 780  
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 ggctggtcag ccacagtgcc gtcaggcccc accaaggggc tctggtggag aggattatcc 960  
 cacacccct ctacagtgcc cagaatcatg actacgacgt cgccctcctg aggctccaga 1020  
 ccgctctcaa cttctcagac actgtgggcg ctgtgtgcct gccggccaag gaacagcatt 1080  
 ttccgaaggg ctgcggtgc tgggtgtctg gctggggcca caccaccct agccatactt 1140  
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Cura 468 SEQ list 0405.txt

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<210> 26

<211> 1787

<212> DNA

<213> Homo sapiens

<400> 26

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tggtagatct gggatacaaa ctcaggcata ctcttaccga gttcatcctt aaactgatag 180  
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tcctagcacc ctccccagtc cccagcaggg cccgggccta aggggtaagg ttccttgcat 300  
tcgagggcag gtcctttaga aatctccctg ccctactcct gccccacac tcacctgagc 360  
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ctctgcgcag ccacgcccc agctgaccac cccactagg cgccatgtgt ccccatctgg 480  
gcacactagg gggccccgcg tatctccctg gcatgcatca gcccttcctg ccaggtagcc 540  
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Cura 468 SEQ list 0405.txt

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<210> 27

<211> 472

<212> PRT

<213> Homo sapiens

<400> 27

## Cura 468 SEQ list 0405.txt

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Gln	His	Pro 35	Ile	Ser	Gln	Ala	Val 40	Cys	Trp	Arg	Ser	Met 45	Arg	Arg	Gly
Cys	Ala 50	Val	Leu	Gly	Ala	Leu 55	Gly	Leu	Leu	Ala	Gly 60	Ala	Gly	Val	Gly
Ser 65	Trp	Leu	Leu	Val	Leu 70	Tyr	Leu	Cys	Pro	Ala 75	Ala	Ser	Gln	Pro	Ile 80
Ser	Gly	Thr	Leu	Gln 85	Asp	Glu	Glu	Ile	Thr 90	Leu	Ser	Cys	Ser	Glu 95	Ala
Ser	Ala	Glu	Glu 100	Ala	Leu	Leu	Pro	Ala 105	Leu	Pro	Lys	Thr	Val 110	Ser	Phe
Arg	Ile	Asn 115	Ser	Glu	Asp	Phe	Leu 120	Leu	Glu	Ala	Gln	Val 125	Arg	Asp	Gln
Pro	Arg 130	Trp	Leu	Leu	Val	Cys 135	His	Glu	Gly	Trp	Ser 140	Pro	Ala	Leu	Gly
Leu 145	Gln	Ile	Cys	Trp	Ser 150	Leu	Gly	His	Leu	Arg 155	Leu	Thr	His	His	Lys 160
Gly	Val	Asn	Leu	Thr 165	Asp	Ile	Lys	Leu	Asn 170	Ser	Ser	Gln	Glu	Phe 175	Ala
Gln	Leu	Ser	Pro 180	Arg	Leu	Gly	Gly	Phe 185	Leu	Glu	Glu	Ala	Trp 190	Gln	Pro
Ser	Arg	Thr 195	Thr	Glu	Ala	Val	Arg 200	Asn	Asn	Cys	Thr	Ser 205	Gly	Gln	Val
Val	Ser 210	Leu	Arg	Cys	Ser	Glu 215	Cys	Gly	Ala	Arg	Pro 220	Leu	Ala	Ser	Arg
Ile 225	Val	Gly	Gly	Gln	Ser 230	Val	Ala	Pro	Gly	Arg 235	Trp	Pro	Trp	Gln	Ala 240
Ser	Val	Ala	Leu	Gly 245	Phe	Arg	His	Thr	Cys 250	Gly	Gly	Ser	Val	Leu 255	Ala



Cura 468 SEQ list 0405.txt

Pro	Arg	Trp	Val	Val	Thr	Ala	Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu
			260					265					270		
Ala	Arg	Leu	Ser	Ser	Trp	Arg	Val	His	Ala	Gly	Leu	Val	Ser	His	Ser
		275					280					285			
Ala	Val	Arg	Pro	His	Gln	Gly	Ala	Leu	Val	Glu	Arg	Ile	Ile	Pro	His
	290					295					300				
Pro	Leu	Tyr	Ser	Ala	Gln	Asn	His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Arg
305					310					315					320
Leu	Gln	Thr	Ala	Leu	Asn	Phe	Ser	Asp	Thr	Val	Gly	Ala	Val	Cys	Leu
				325					330					335	
Pro	Ala	Lys	Glu	Gln	His	Phe	Pro	Lys	Gly	Ser	Arg	Cys	Trp	Val	Ser
			340					345					350		
Gly	Trp	Gly	His	Thr	His	Pro	Ser	His	Thr	Tyr	Ser	Ser	Asp	Met	Leu
		355					360					365			
Gln	Asp	Thr	Val	Val	Pro	Leu	Leu	Ser	Thr	Gln	Leu	Cys	Asn	Ser	Ser
	370					375					380				
Cys	Val	Tyr	Ser	Gly	Ala	Leu	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	Tyr
385					390					395					400
Leu	Asp	Gly	Arg	Ala	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu
				405					410					415	
Val	Cys	Pro	Asp	Gly	Asp	Thr	Trp	Arg	Leu	Val	Gly	Val	Val	Ser	Trp
			420					425					430		
Gly	Arg	Gly	Cys	Ala	Glu	Pro	Asn	His	Pro	Gly	Val	Tyr	Ala	Lys	Val
		435					440					445			
Ala	Glu	Phe	Leu	Asp	Trp	Ile	His	Asp	Thr	Ala	Gln	Val	Ser	Val	Gly
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<211> 2148

<212> DNA

<213> Homo sapiens

## Cura 468 SEQ list 0405.txt

&lt;400&gt; 28

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 ctggagacca gcagcatccc atttctcagg cgggtgtgctg gcgttccatg cgacgtggct 300  
 gtgcagtgct gggagccctg gggctgctgg ccggtgcagg tgttggctca tggctcctag 360  
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 taactttgag ctgctcagag gccagcgtg aggaagctct gctccctgca ctccccaaaa 480  
 cagtatcttt cagaataaac agcgaagact tcttgctgga agcgcaagtg agggatcagc 540  
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 gccacacca ccctagccat acttacagct cggatatgct ccaggacacg gtggtgcccc 1140  
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 gctgcgcaga gcccaatcac ccagggtgtct acgccaaggt agctgagttt ctggactgga 1380  
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Cura 468 SEQ list 0405.txt

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agcctccgac acagaacgca tggacctcct actactgtgt gtgaggaaca gtcactaccc 1560
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			20					25					30		
Gln	His	Pro	Ile	Ser	Gln	Ala	Val	Cys	Trp	Arg	Ser	Met	Arg	Arg	Gly
		35					40					45			
Cys	Ala	Val	Leu	Gly	Ala	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Val	Gly
	50					55					60				
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Cys	Pro	Ala	Ala	Ser	Gln	Pro	Ile
65					70					75					80

Cura 468 SEQ list 0405.txt

Ser	Gly	Thr	Leu	Gln	Asp	Glu	Glu	Ile	Thr	Leu	Ser	Cys	Ser	Glu	Ala	
				85					90					95		
Ser	Ala	Glu	Glu	Ala	Leu	Leu	Pro	Ala	Leu	Pro	Lys	Thr	Val	Ser	Phe	
			100					105					110			
Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln	
		115					120					125				
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly	
	130					135					140					
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys	
145					150					155					160	
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala	
				165					170					175		
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro	
			180					185					190			
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu	
		195					200					205				
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val	
	210					215					220					
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg	
225					230					235					240	
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala	
				245					250					255		
Ala	His	Cys	Met	His	Ser	Ala	Gln	Asn	His	Asp	Tyr	Asp	Val	Ala	Leu	
			260					265					270			
Leu	Arg	Leu	Gln	Thr	Ala	Leu	Asn	Phe	Ser	Asp	Thr	Val	Gly	Ala	Val	
		275					280					285				
Cys	Leu	Pro	Ala	Lys	Glu	Gln	His	Phe	Pro	Lys	Gly	Ser	Arg	Cys	Trp	
	290					295					300					
Val	Ser	Gly	Trp	Cys	His	Thr	His	Pro	Ser	His	Thr	Tyr	Ser	Ser	Asp	
305					310					315					320	
Met	Leu	Gln	Asp	Thr	Val	Val	Pro	Leu	Leu	Ser	Thr	Gln	Leu	Cys	Asn	
				325					330					335		

Cura 468 SEQ list 0405.txt

Ser Ser Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala  
340 345 350

Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly  
355 360 365

Pro Leu Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val  
370 375 380

Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala  
385 390 395 400

Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Asp Ser  
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Leu Leu

<210> 30

<211> 1593

<212> PRT

<213> Homo sapiens

<400> 30

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Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly  
35 40 45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly  
50 55 60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg  
65 70 75 80

Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser  
85 90 95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe  
100 105 110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His  
115 120 125

Cura 468 SEQ list 0405.txt

Val	Lys	Met	Met	Ala	Ser	Ser	Ala	Pro	Leu	Cys	His	Leu	Ser	Gly	Thr	130	135	140	
Val	Leu	Gln	Gln	Gly	Thr	Arg	Val	Gly	Thr	Ala	Ala	Leu	Ser	Ala	Cys	145	150	155	160
His	Gly	Leu	Thr	Gly	Phe	Phe	Gln	Leu	Pro	His	Gly	Asp	Phe	Phe	Ile	165	170	175	
Glu	Pro	Val	Lys	Lys	His	Pro	Leu	Val	Glu	Gly	Gly	Tyr	His	Pro	His	180	185	190	
Ile	Val	Tyr	Arg	Arg	Gln	Lys	Val	Pro	Glu	Thr	Lys	Glu	Pro	Thr	Cys	195	200	205	
Gly	Leu	Lys	Asp	Ser	Val	Asn	Ile	Ser	Gln	Lys	Gln	Glu	Leu	Trp	Arg	210	215	220	
Glu	Lys	Trp	Glu	Arg	His	Asn	Leu	Pro	Ser	Arg	Ser	Leu	Ser	Arg	Arg	225	230	235	240
Ser	Ile	Ser	Lys	Glu	Arg	Trp	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Thr	245	250	255	
Lys	Met	Ile	Glu	Tyr	His	Gly	Ser	Glu	Asn	Val	Glu	Ser	Tyr	Ile	Leu	260	265	270	
Thr	Ile	Met	Asn	Met	Val	Thr	Gly	Leu	Phe	His	Asn	Pro	Ser	Ile	Gly	275	280	285	
Asn	Ala	Ile	His	Ile	Val	Val	Val	Arg	Leu	Ile	Leu	Leu	Glu	Glu	Glu	290	295	300	
Glu	Gln	Gly	Leu	Lys	Ile	Val	His	His	Ala	Glu	Lys	Thr	Leu	Ser	Ser	305	310	315	320
Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Asn	Pro	Lys	Ser	Asp	Leu	Asn	Pro	325	330	335	
Val	His	His	Asp	Val	Ala	Val	Leu	Leu	Thr	Arg	Lys	Asp	Ile	Cys	Ala	340	345	350	
Gly	Phe	Asn	Arg	Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Leu	Ser	Gly	355	360	365	
Met	Cys	Gln	Pro	His	Arg	Ser	Cys	Asn	Ile	Asn	Glu	Asp	Ser	Gly	Leu	370	375	380	

Cura 468 SEQ list 0405.txt

Pro	Leu	Ala	Phe	Thr	Ile	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	385	390	395	400
Gln	His	Asp	Gly	Lys	Glu	Asn	Asp	Cys	Glu	Pro	Val	Gly	Arg	His	Pro	405	410	415	
Tyr	Ile	Met	Ser	Arg	Gln	Leu	Gln	Tyr	Asp	Pro	Thr	Pro	Leu	Thr	Trp	420	425	430	
Ser	Lys	Cys	Ser	Glu	Glu	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp	435	440	445	
Gly	Phe	Cys	Leu	Asp	Asp	Ile	Pro	Lys	Lys	Lys	Gly	Leu	Lys	Ser	Lys	450	455	460	
Val	Ile	Ala	Pro	Gly	Val	Ile	Tyr	Asp	Val	His	His	Gln	Cys	Gln	Leu	465	470	475	480
Gln	Tyr	Gly	Pro	Asn	Ala	Thr	Phe	Cys	Gln	Glu	Val	Glu	Asn	Val	Cys	485	490	495	
Gln	Thr	Leu	Trp	Cys	Ser	Val	Lys	Gly	Phe	Cys	Arg	Ser	Lys	Leu	Asp	500	505	510	
Ala	Ala	Ala	Asp	Gly	Thr	Gln	Cys	Gly	Glu	Lys	Lys	Trp	Cys	Met	Ala	515	520	525	
Gly	Lys	Cys	Ile	Thr	Val	Gly	Lys	Lys	Pro	Glu	Ser	Ile	Pro	Gly	Gly	530	535	540	
Trp	Gly	Arg	Trp	Ser	Pro	Trp	Ser	His	Cys	Ser	Arg	Thr	Cys	Gly	Ala	545	550	555	560
Gly	Val	Gln	Ser	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Pro	Glu	Pro	Lys	Phe	565	570	575	
Gly	Gly	Lys	Tyr	Cys	Thr	Gly	Glu	Arg	Lys	Arg	Tyr	Arg	Leu	Cys	Asn	580	585	590	
Val	His	Pro	Cys	Arg	Ser	Glu	Ala	Pro	Thr	Phe	Arg	Gln	Met	Gln	Cys	595	600	605	
Ser	Glu	Phe	Asp	Thr	Val	Pro	Tyr	Lys	Asn	Glu	Leu	Tyr	His	Trp	Phe	610	615	620	
Pro	Ile	Phe	Asn	Pro	Ala	His	Pro	Cys	Glu	Leu	Tyr	Cys	Arg	Pro	Ile	625	630	635	640

Cura 468 SEQ list 0405.txt

Asp	Gly	Gln	Phe	Ser	Glu	Lys	Met	Leu	Asp	Ala	Val	Ile	Asp	Gly	Thr	645	650	655
Pro	Cys	Phe	Glu	Gly	Gly	Asn	Ser	Arg	Asn	Val	Cys	Ile	Asn	Gly	Ile	660	665	670
Cys	Lys	Met	Val	Gly	Cys	Asp	Tyr	Glu	Ile	Asp	Ser	Asn	Ala	Thr	Glu	675	680	685
Asp	Arg	Cys	Gly	Val	Cys	Leu	Gly	Asp	Gly	Ser	Ser	Cys	Gln	Thr	Val	690	695	700
Arg	Lys	Met	Phe	Lys	Gln	Lys	Glu	Gly	Ser	Gly	Tyr	Val	Asp	Ile	Gly	705	710	715
Leu	Ile	Pro	Lys	Gly	Ala	Arg	Asp	Ile	Arg	Val	Met	Glu	Ile	Glu	Gly	725	730	735
Ala	Gly	Asn	Phe	Leu	Ala	Ile	Arg	Ser	Glu	Asp	Pro	Glu	Lys	Tyr	Tyr	740	745	750
Leu	Asn	Gly	Gly	Phe	Ile	Ile	Gln	Trp	Asn	Gly	Asn	Tyr	Lys	Leu	Ala	755	760	765
Gly	Thr	Val	Phe	Gln	Tyr	Asp	Arg	Lys	Gly	Asp	Leu	Glu	Lys	Leu	Met	770	775	780
Ala	Thr	Gly	Pro	Thr	Asn	Glu	Ser	Val	Trp	Ile	Gln	Leu	Leu	Phe	Gln	785	790	795
Val	Thr	Asn	Pro	Gly	Ile	Lys	Tyr	Glu	Tyr	Thr	Ile	Gln	Lys	Asp	Gly	805	810	815
Leu	Asp	Asn	Asp	Val	Glu	Gln	Met	Tyr	Phe	Trp	Gln	Tyr	Gly	His	Trp	820	825	830
Thr	Glu	Cys	Ser	Val	Thr	Cys	Gly	Thr	Gly	Ile	Arg	Arg	Gln	Thr	Ala	835	840	845
His	Cys	Ile	Lys	Lys	Gly	Arg	Gly	Met	Val	Lys	Ala	Thr	Phe	Cys	Asp	850	855	860
Pro	Glu	Thr	Gln	Pro	Asn	Gly	Arg	Gln	Lys	Lys	Cys	His	Glu	Lys	Ala	865	870	875
Cys	Pro	Pro	Arg	Trp	Trp	Ala	Gly	Glu	Trp	Glu	Ala	Cys	Ser	Ala	Thr	885	890	895



Cura 468 SEQ list 0405.txt

Cys	Gly	Pro	His	Gly	Glu	Lys	Lys	Arg	Thr	Val	Leu	Cys	Ile	Gln	Thr		
			900					905					910				
Met	Val	Ser	Asp	Glu	Gln	Ala	Leu	Pro	Pro	Thr	Asp	Cys	Gln	His	Leu		
		915					920					925					
Leu	Lys	Pro	Lys	Thr	Leu	Leu	Ser	Cys	Asn	Arg	Asp	Ile	Leu	Cys	Pro		
	930					935					940						
Ser	Asp	Trp	Thr	Val	Gly	Asn	Trp	Ser	Glu	Cys	Ser	Val	Ser	Cys	Gly		
945					950					955					960		
Gly	Gly	Val	Arg	Ile	Arg	Ser	Val	Thr	Cys	Ala	Lys	Asn	His	Asp	Glu		
				965					970					975			
Pro	Cys	Asp	Val	Thr	Arg	Lys	Pro	Asn	Ser	Arg	Ala	Leu	Cys	Gly	Leu		
			980					985					990				
Gln	Gln	Cys	Pro	Ser	Ser	Arg	Arg	Val	Leu	Lys	Pro	Asn	Lys	Gly	Thr		
		995					1000					1005					
Ile	Ser	Asn	Gly	Lys	Asn	Pro	Pro	Thr	Leu	Lys	Pro	Val	Pro	Pro	Pro		
	1010					1015					1020						
Thr	Ser	Arg	Pro	Arg	Met	Leu	Thr	Thr	Pro	Thr	Gly	Pro	Glu	Ser	Met		
1025					1030					1035					1040		
Ser	Thr	Ser	Thr	Pro	Ala	Ile	Ser	Ser	Pro	Ser	Pro	Thr	Thr	Ala	Ser		
				1045					1050					1055			
Lys	Glu	Gly	Asp	Leu	Gly	Gly	Lys	Gln	Trp	Gln	Asp	Ser	Ser	Thr	Gln		
			1060					1065					1070				
Pro	Glu	Leu	Ser	Ser	Arg	Tyr	Leu	Ile	Ser	Thr	Gly	Ser	Thr	Ser	Gln		
	1075						1080					1085					
Pro	Ile	Leu	Thr	Ser	Gln	Ser	Leu	Ser	Ile	Gln	Pro	Ser	Glu	Glu	Asn		
	1090					1095					1100						
Val	Ser	Ser	Ser	Asp	Thr	Gly	Pro	Thr	Ser	Glu	Gly	Gly	Leu	Val	Ala		
1105					1110					1115					1120		
Thr	Thr	Thr	Ser	Gly	Ser	Gly	Leu	Ser	Ser	Ser	Arg	Asn	Pro	Ile	Thr		
				1125					1130					1135			
Trp	Pro	Val	Thr	Pro	Phe	Tyr	Asn	Thr	Leu	Thr	Lys	Gly	Pro	Glu	Met		
			1140					1145					1150				

Cura 468 SEQ list 0405.txt

Glu Ile His Ser Gly Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp Lys  
1155 1160 1165

Asp Glu Ser Asn Pro Val Ile Trp Thr Lys Ile Arg Val Pro Gly Asn  
1170 1175 1180

Asp Ala Pro Val Glu Ser Thr Glu Met Pro Leu Ala Pro Pro Leu Thr  
1185 1190 1195 1200

Pro Asp Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe Ser Thr Val Met  
1205 1210 1215

Glu Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr Ser Glu Thr Gly Thr  
1220 1225 1230

Pro Arg Val Glu Gly Met Val Thr Glu Lys Pro Ala Asn Thr Leu Leu  
1235 1240 1245

Pro Leu Gly Gly Asp His Gln Pro Glu Pro Ser Gly Lys Thr Ala Asn  
1250 1255 1260

Arg Asn His Leu Lys Leu Pro Asn Asn Met Asn Gln Thr Lys Ser Ser  
1265 1270 1275 1280

Glu Pro Val Leu Thr Glu Glu Asp Ala Thr Ser Leu Ile Thr Glu Gly  
1285 1290 1295

Phe Leu Leu Asn Ala Ser Asn Tyr Lys Gln Leu Thr Asn Gly His Gly  
1300 1305 1310

Ser Ala His Trp Ile Val Gly Asn Trp Ser Glu Cys Ser Thr Thr Cys  
1315 1320 1325

Gly Leu Gly Ala Tyr Trp Lys Arg Val Glu Cys Thr Thr Gln Met Asp  
1330 1335 1340

Ser Asp Cys Ala Ala Ile Gln Arg Pro Asp Pro Ala Lys Arg Cys His  
1345 1350 1355 1360

Leu Arg Pro Cys Ala Gly Trp Lys Val Gly Asn Trp Ser Lys Cys Ser  
1365 1370 1375

Arg Asn Cys Ser Gly Gly Phe Lys Ile Arg Glu Ile Gln Cys Val Asp  
1380 1385 1390

Ser Arg Asp His Arg Asn Leu Arg Pro Phe His Cys Gln Phe Leu Ala  
1395 1400 1405

Cura 468 SEQ list 0405.txt

Gly Ile Pro Pro Pro Leu Ser Met Ser Cys Asn Pro Glu Pro Cys Glu  
1410 1415 1420

Ala Trp Gln Val Glu Pro Trp Ser Gln Cys Ser Arg Ser Cys Gly Gly  
1425 1430 1435 1440

Gly Val Gln Glu Arg Gly Val Phe Cys Pro Gly Gly Leu Cys Asp Trp  
1445 1450 1455

Thr Lys Arg Pro Thr Ser Thr Met Ser Cys Asn Glu His Leu Cys Cys  
1460 1465 1470

His Trp Ala Thr Gly Asn Trp Asp Leu Cys Ser Thr Ser Cys Gly Gly  
1475 1480 1485

Gly Phe Gln Lys Arg Ile Val Gln Cys Val Pro Ser Glu Gly Asn Lys  
1490 1495 1500

Thr Glu Asp Gln Asp Gln Cys Leu Cys Asp His Lys Pro Arg Pro Pro  
1505 1510 1515 1520

Glu Phe Lys Lys Cys Asn Gln Gln Ala Cys Lys Lys Ser Ala Asp Leu  
1525 1530 1535

Leu Cys Thr Lys Asp Lys Leu Ser Ala Ser Phe Cys Gln Thr Leu Lys  
1540 1545 1550

Ala Met Lys Lys Cys Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe  
1555 1560 1565

Ser Cys Pro Gln Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln  
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Arg Leu Leu Gln Lys Ser Lys Glu Leu  
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Phe Pro Thr Arg Val Asp His Asn Gly Ala Leu Leu Ala Phe Ser Pro

[illegible]

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## Cura 468 SEQ list 0405.txt

275		280		285
Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn Ala				
290		295		300
Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile Thr				
305		310		315
Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu Gly				
		325		330
Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser Val				
		340		345
Asn Glu Asp Ile Gly Leu Pro Gln Ala Phe Thr Ile Ala His Glu Ile				
		355		360
Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys Gly				
		370		375
Ala Arg Gly Gln Asp Pro Ala Lys Leu Met Ala Ala His Ile Thr Met				
385		390		395
Lys Thr Asn Pro Phe Val Trp Ser Ser Cys Asn Arg Asp Tyr Ile Thr				
		405		410
Ser Phe Leu Asp Ser Gly Leu Gly Leu Cys Leu Asn Asn Arg Pro Pro				
		420		425
Arg Gln Asp Phe Val Tyr Pro Thr Val Ala Pro Gly Gln Ala Tyr Asp				
		435		440
Ala Asp Glu Gln Cys Arg Phe Gln His Gly Val Lys Ser Arg Gln Cys				
		450		455
Lys Tyr Gly Glu Val Cys Ser Glu Leu Trp Cys Leu Ser Lys Ser Asn				
465		470		475
Arg Cys Ile Thr Asn Ser Ile Pro Ala Ala Glu Gly Thr Leu Cys Gln				
		485		490
Thr His Thr Ile Asp Lys Gly Trp Cys Tyr Lys Arg Val Cys Val Pro				
		500		505
Phe Gly Ser Arg Pro Glu Gly Val Asp Gly Ala Trp Gly Pro Trp Thr				
		515		520
Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Ser Ser Ser				

Cura 468 SEQ list 0405.txt

530

535

540

Ser	Arg	His	Cys	Asp	Ser	Pro	Arg	Pro	Thr	Ile	Gly	Gly	Lys	Tyr	Cys
545					550					555					560
Leu	Gly	Glu	Arg	Arg	Arg	His	Arg	Ser	Cys	Asn	Thr	Asp	Asp	Cys	Pro
				565					570					575	
Pro	Gly	Ser	Gln	Asp	Phe	Arg	Glu	Val	Gln	Cys	Ser	Glu	Phe	Asp	Ser
			580					585					590		
Ile	Pro	Phe	Arg	Gly	Lys	Phe	Tyr	Lys	Trp	Lys	Thr	Tyr	Arg	Gly	Gly
		595					600					605			
Gly	Val	Lys	Ala	Cys	Ser	Leu	Thr	Ser	Leu	Ala	Glu	Gly	Phe	Asn	Phe
	610					615					620				
Tyr	Thr	Glu	Arg	Ala	Ala	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Arg	Pro
625					630					635					640
Asp	Thr	Val	Asp	Ile	Cys	Val	Ser	Gly	Glu	Cys	Lys	His	Val	Gly	Cys
				645					650					655	
Asp	Arg	Val	Leu	Gly	Ser	Asp	Leu	Arg	Glu	Asp	Lys	Cys	Arg	Val	Cys
			660					665					670		
Gly	Gly	Asp	Gly	Ser	Ala	Cys	Glu	Thr	Ile	Glu	Gly	Val	Phe	Ser	Pro
		675					680					685			
Ala	Ser	Pro	Gly	Ala	Gly	Tyr	Glu	Asp	Val	Val	Trp	Ile	Pro	Lys	Gly
	690					695					700				
Ser	Val	His	Ile	Phe	Ile	Gln	Asp	Leu	Asn	Leu	Ser	Leu	Ser	His	Leu
705					710					715					720
Ala	Leu	Lys	Gly	Asp	Gln	Glu	Ser	Leu	Leu	Leu	Glu	Gly	Leu	Pro	Gly
				725					730					735	
Thr	Pro	Gln	Pro	His	Arg	Leu	Pro	Leu	Ala	Gly	Thr	Thr	Phe	Gln	Leu
			740					745					750		
Arg	Gln	Gly	Pro	Asp	Gln	Val	Gln	Ser	Leu	Glu	Ala	Leu	Gly	Pro	Ile
		755					760					765			
Asn	Ala	Ser	Leu	Ile	Val	Met	Val	Leu	Ala	Arg	Thr	Glu	Leu	Pro	Ala
	770					775					780				
Leu	Arg	Tyr	Arg	Phe	Asn	Ala	Pro	Ile	Ala	Arg	Asp	Ser	Leu	Pro	Pro

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785					790					795						800
Tyr	Ser	Trp	His	Tyr	Ala	Pro	Trp	Thr	Lys	Cys	Ser	Ala	Gln	Cys	Ala	
				805					810					815		
Gly	Gly	Ser	Gln	Val	Gln	Ala	Val	Glu	Cys	Arg	Asn	Gln	Leu	Asp	Ser	
			820					825					830			
Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	Lys	
		835					840					845				
Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	Val	
	850					855					860					
Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	Ser	
865					870					875					880	
Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	Ala	
				885					890					895		
Leu	Asp	Asp	Ser	Ala	Cys	Pro	Gln	Pro	Arg	Pro	Pro	Val	Leu	Glu	Ala	
			900					905					910			
Cys	His	Gly	Pro	Thr	Cys	Pro	Pro	Glu	Trp	Ala	Ala	Leu	Asp	Trp	Ser	
		915					920					925				
Glu	Cys	Thr	Pro	Ser	Cys	Gly	Pro	Gly	Leu	Arg	His	Arg	Val	Val	Leu	
	930					935					940					
Cys	Lys	Ser	Ala	Asp	His	Arg	Ala	Thr	Leu	Pro	Pro	Ala	His	Cys	Ser	
945					950					955					960	
Pro	Ala	Ala	Lys	Pro	Pro	Ala	Thr	Met	Arg	Cys	Asn	Leu	Arg	Arg	Cys	
				965					970					975		
Pro	Pro	Ala	Arg	Trp	Val	Ala	Gly	Glu	Trp	Gly	Glu	Cys	Ser	Ala	Gln	
			980					985					990			
Cys	Gly	Val	Gly	Gln	Arg	Gln	Arg	Ser	Val	Arg	Cys	Thr	Ser	His	Thr	
		995					1000					1005				
Gly	Gln	Ala	Ser	His	Glu	Cys	Thr	Glu	Ala	Leu	Arg	Pro	Pro	Thr	Thr	
	1010						1015				1020					
Gln	Gln	Cys	Glu	Ala	Lys	Cys	Asp	Ser	Pro	Thr	Pro	Gly	Asp	Gly	Pro	
1025					1030					1035					1040	
Glu	Glu	Cys	Lys	Asp	Val	Asn	Lys	Val	Ala	Tyr	Cys	Pro	Leu	Val	Leu	

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1045

1050

1055

Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys Lys  
1060 1065 1070

Thr Cys Gln Gly His  
1075

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<211> 997  
<212> PRT  
<213> Homo sapiens

<400> 32  
Met Pro Gly Gly Pro Ser Pro Arg Ser Pro Ala Pro Leu Leu Arg Pro  
1 5 10 15

Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala  
20 25 30

Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro  
35 40 45

Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro  
50 55 60

Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala  
65 70 75 80

Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr  
85 90 95

Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg  
100 105 110

Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys  
115 120 125

His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala  
130 135 140

Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn  
145 150 155 160

Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly  
165 170 175



Cura 468 SEQ list 0405.txt

His	Ala	Gln	Pro	His	Val	Val	Tyr	Lys	Arg	Gln	Ala	Pro	Glu	Arg	Leu	180	185	190
Ala	Gln	Arg	Gly	Asp	Ser	Ser	Ala	Pro	Ser	Thr	Cys	Gly	Val	Gln	Val	195	200	205
Tyr	Pro	Glu	Leu	Glu	Ser	Arg	Arg	Glu	Arg	Trp	Glu	Gln	Arg	Gln	Gln	210	215	220
Trp	Arg	Arg	Pro	Arg	Leu	Arg	Arg	Leu	His	Gln	Arg	Ser	Val	Ser	Lys	225	230	235
Glu	Lys	Trp	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Ala	Lys	Met	Val	Glu	245	250	255
Tyr	His	Gly	Gln	Pro	Gln	Val	Glu	Ser	Tyr	Val	Leu	Thr	Ile	Met	Asn	260	265	270
Met	Val	Ala	Gly	Leu	Phe	His	Asp	Pro	Ser	Ile	Gly	Asn	Pro	Ile	His	275	280	285
Ile	Thr	Ile	Val	Arg	Leu	Val	Leu	Leu	Glu	Asp	Glu	Glu	Glu	Asp	Leu	290	295	300
Lys	Ile	Thr	His	His	Ala	Asp	Asn	Thr	Leu	Lys	Ser	Phe	Cys	Lys	Trp	305	310	315
Gln	Lys	Ser	Ile	Asn	Met	Lys	Gly	Asp	Ala	His	Pro	Leu	His	His	Asp	325	330	335
Thr	Ala	Ile	Leu	Leu	Thr	Arg	Lys	Asp	Leu	Cys	Ala	Ala	Met	Asn	Arg	340	345	350
Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Val	Ala	Gly	Met	Cys	Gln	Pro	355	360	365
His	Arg	Ser	Cys	Ser	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Pro	Leu	Ala	Phe	370	375	380
Thr	Val	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	Gln	His	Asp	Gly	385	390	395
Ser	Gly	Asn	Asp	Cys	Glu	Pro	Val	Gly	Lys	Arg	Pro	Phe	Ile	Met	Ser	405	410	415
Pro	Gln	Leu	Leu	Tyr	Asp	Ala	Ala	Pro	Leu	Thr	Trp	Ser	Arg	Cys	Ser	420	425	430

Cura 468 SEQ list 0405.txt

Arg	Gln	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp	Gly	Leu	Cys	Leu	435	440	445
Asp	Asp	Pro	Pro	Ala	Lys	Asp	Ile	Ile	Asp	Phe	Pro	Ser	Val	Pro	Pro	450	455	460
Gly	Val	Leu	Tyr	Asp	Val	Ser	His	Gln	Cys	Arg	Leu	Gln	Tyr	Gly	Ala	465	470	475
Tyr	Ser	Ala	Phe	Cys	Glu	Asp	Met	Asp	Asn	Val	Cys	His	Thr	Leu	Trp	485	490	495
Cys	Ser	Val	Gly	Thr	Thr	Cys	His	Ser	Lys	Leu	Asp	Ala	Ala	Val	Asp	500	505	510
Gly	Thr	Arg	Cys	Gly	Glu	Asn	Lys	Trp	Cys	Leu	Ser	Gly	Glu	Cys	Val	515	520	525
Pro	Val	Gly	Phe	Arg	Pro	Glu	Ala	Val	Asp	Gly	Gly	Trp	Ser	Gly	Trp	530	535	540
Ser	Ala	Trp	Ser	Ile	Cys	Ser	Arg	Ser	Cys	Gly	Met	Gly	Val	Gln	Ser	545	550	555
Ala	Glu	Arg	Gln	Cys	Thr	Gln	Pro	Thr	Pro	Lys	Tyr	Lys	Gly	Arg	Tyr	565	570	575
Cys	Val	Gly	Glu	Arg	Lys	Arg	Phe	Arg	Leu	Cys	Asn	Leu	Gln	Ala	Cys	580	585	590
Pro	Ala	Gly	Arg	Pro	Ser	Phe	Arg	His	Val	Gln	Cys	Ser	His	Phe	Asp	595	600	605
Ala	Met	Leu	Tyr	Lys	Gly	Gln	Leu	His	Thr	Trp	Val	Pro	Val	Val	Asn	610	615	620
Asp	Val	Asn	Pro	Cys	Glu	Leu	His	Cys	Arg	Pro	Ala	Asn	Glu	Tyr	Phe	625	630	635
Ala	Lys	Lys	Leu	Arg	Asp	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Tyr	Gln	645	650	655
Val	Arg	Ala	Ser	Arg	Asp	Leu	Cys	Ile	Asn	Gly	Ile	Cys	Lys	Asn	Val	660	665	670
Gly	Cys	Asp	Phe	Glu	Ile	Asp	Ser	Gly	Ala	Met	Glu	Asp	Arg	Cys	Gly	675	680	685

Cura 468 SEQ list 0405.txt

Val	Cys	His	Gly	Asn	Gly	Ser	Thr	Cys	His	Thr	Val	Ser	Gly	Thr	Phe
690						695					700				
Glu	Glu	Ala	Glu	Gly	Leu	Gly	Tyr	Val	Asp	Val	Gly	Leu	Ile	Pro	Ala
705					710					715					720
Gly	Ala	Arg	Glu	Ile	Arg	Ile	Gln	Glu	Val	Ala	Glu	Ala	Ala	Asn	Phe
				725					730					735	
Leu	Ala	Leu	Arg	Ser	Glu	Asp	Pro	Glu	Lys	Tyr	Phe	Leu	Asn	Gly	Gly
			740					745					750		
Trp	Thr	Ile	Gln	Trp	Asn	Gly	Asp	Tyr	Gln	Val	Ala	Gly	Thr	Thr	Phe
		755					760					765			
Thr	Tyr	Ala	Arg	Arg	Gly	Asn	Trp	Glu	Asn	Leu	Thr	Ser	Pro	Gly	Pro
	770					775					780				
Thr	Lys	Glu	Pro	Val	Trp	Ile	Gln	Val	Pro	Ala	Ser	Arg	Gly	Pro	Gly
785					790					795					800
Gly	Gly	Ser	Arg	Gly	Gly	Val	Pro	Arg	Pro	Ser	Thr	Leu	His	Gly	Arg
				805					810					815	
Ser	Arg	Pro	Gly	Gly	Val	Ser	Pro	Gly	Ser	Val	Thr	Glu	Pro	Gly	Ser
			820					825					830		
Glu	Pro	Gly	Pro	Pro	Ala	Ala	Ala	Ser	Thr	Ser	Val	Ser	Pro	Ser	Leu
		835					840					845			
Lys	Trp	Pro	Asn	Leu	Val	Ala	Ala	Val	His	Arg	Gly	Gly	Trp	Gly	Gln
	850					855					860				
Ala	Pro	Leu	Gly	Leu	Gly	Gly	Trp	Arg	Arg	His	Leu	Val	Leu	Met	Gly
865					870					875					880
Pro	Arg	Leu	Pro	Thr	Gln	Leu	Leu	Phe	Gln	Glu	Ser	Asn	Pro	Gly	Val
				885					890					895	
His	Tyr	Glu	Tyr	Thr	Ile	His	Arg	Glu	Ala	Gly	Gly	His	Asp	Glu	Val
			900					905					910		
Pro	Pro	Pro	Val	Phe	Ser	Trp	His	Tyr	Gly	Pro	Trp	Thr	Lys	Cys	Thr
		915					920					925			
Val	Thr	Cys	Gly	Arg	Gly	Glu	Lys	Trp	Gly	Arg	His	Ser	Pro	Thr	Cys
	930					935					940				

Cura 468 SEQ list 0405.txt

Arg Gly Leu Val Ser Gly Gln Gly His Trp Leu Gln Leu Pro Ala His  
945 950 955 960

Cys Trp Ala Thr Thr Gly Leu Glu Val Cys Phe Ser Glu Pro Gln Phe  
965 970 975

Ser Ile Cys Glu Met Arg Leu Ala Ile Ala Leu Cys Pro Arg Pro Ala  
980 985 990

Gly Arg Val His Gly  
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<210> 33

<211> 854

<212> PRT

<213> Homo sapiens

<400> 33

Met Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu  
1 5 10 15

Ala Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly  
20 25 30

Ser Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp  
35 40 45

Gln Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser  
50 55 60

Phe Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn  
65 70 75 80

Ala Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile  
85 90 95

Thr Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu  
100 105 110

Gly Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser  
115 120 125

Val Asn Glu Asp Ile Gly Leu Ala Thr Ala Phe Thr Ile Ala His Glu  
130 135 140

Ile Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys  
145 150 155 160

Cura 468 SEQ list 0405.txt

Gly	Ala	Arg	Gly	Gln	Asp	Pro	Ala	Lys	Leu	Met	Ala	Ala	His	Ile	Thr	165	170	175
Met	Lys	Thr	Asn	Pro	Phe	Val	Trp	Ser	Ser	Cys	Ser	Arg	Asp	Tyr	Ile	180	185	190
Thr	Ser	Phe	Leu	Asp	Ser	Gly	Leu	Gly	Leu	Cys	Leu	Asn	Asn	Arg	Pro	195	200	205
Pro	Arg	Gln	Asp	Phe	Val	Tyr	Pro	Thr	Val	Ala	Pro	Gly	Gln	Ala	Tyr	210	215	220
Asp	Ala	Asp	Glu	Gln	Cys	Arg	Phe	Gln	His	Gly	Val	Lys	Ser	Arg	Gln	225	230	235
Cys	Lys	Tyr	Gly	Glu	Val	Cys	Ser	Glu	Leu	Trp	Cys	Leu	Ser	Lys	Ser	245	250	255
Asn	Arg	Cys	Ile	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	Gly	Thr	Leu	Cys	260	265	270
Gln	Thr	His	Thr	Ile	Asp	Lys	Gly	Trp	Cys	Tyr	Lys	Arg	Val	Cys	Val	275	280	285
Pro	Phe	Gly	Ser	Arg	Pro	Glu	Gly	Val	Asp	Gly	Ala	Trp	Gly	Pro	Trp	290	295	300
Thr	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	Ser	305	310	315
Ser	Ser	Arg	His	Cys	Asp	Ser	Pro	Arg	Pro	Thr	Ile	Gly	Gly	Lys	Tyr	325	330	335
Cys	Leu	Gly	Glu	Arg	Arg	Arg	His	Arg	Ser	Cys	Asn	Thr	Asp	Asp	Cys	340	345	350
Pro	Pro	Gly	Ser	Gln	Asp	Phe	Arg	Glu	Val	Gln	Cys	Ser	Glu	Phe	Asp	355	360	365
Ser	Ile	Pro	Phe	Arg	Gly	Lys	Phe	Tyr	Lys	Trp	Lys	Thr	Tyr	Arg	Gly	370	375	380
Gly	Gly	Val	Lys	Ala	Cys	Ser	Leu	Thr	Cys	Leu	Ala	Glu	Gly	Phe	Asn	385	390	395
Phe	Tyr	Thr	Glu	Arg	Ala	Ala	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Arg	405	410	415

Cura 468 SEQ list 0405.txt

Pro	Asp	Thr	Val	Asp	Ile	Cys	Val	Ser	Gly	Glu	Cys	Lys	His	Val	Gly	
			420					425					430			
Cys	Asp	Arg	Val	Leu	Gly	Ser	Asp	Leu	Arg	Glu	Asp	Lys	Cys	Arg	Val	
		435					440					445				
Cys	Gly	Gly	Asp	Gly	Ser	Ala	Cys	Glu	Thr	Ile	Glu	Gly	Val	Phe	Ser	
	450					455					460					
Pro	Ala	Ser	Pro	Gly	Ala	Gly	Tyr	Glu	Asp	Val	Val	Trp	Ile	Pro	Lys	
465					470					475					480	
Gly	Ser	Val	His	Ile	Phe	Ile	Gln	Asp	Leu	Asn	Leu	Ser	Leu	Ser	His	
				485					490					495		
Leu	Ala	Leu	Lys	Gly	Asp	Gln	Glu	Ser	Leu	Leu	Leu	Glu	Gly	Leu	Pro	
			500					505					510			
Gly	Thr	Pro	Gln	Pro	His	Arg	Leu	Pro	Leu	Ala	Gly	Thr	Thr	Phe	Gln	
		515					520					525				
Leu	Arg	Gln	Gly	Pro	Asp	Gln	Val	Gln	Ser	Leu	Glu	Ala	Leu	Gly	Pro	
	530					535					540					
Ile	Asn	Ala	Ser	Leu	Ile	Val	Met	Val	Leu	Ala	Arg	Thr	Glu	Leu	Pro	
545					550					555					560	
Ala	Leu	Arg	Tyr	Arg	Phe	Asn	Ala	Pro	Ile	Ala	Arg	Asp	Ser	Leu	Pro	
				565					570					575		
Pro	Tyr	Ser	Trp	His	Tyr	Ala	Pro	Trp	Thr	Lys	Cys	Ser	Ala	Gln	Cys	
			580					585					590			
Ala	Gly	Gly	Ser	Gln	Val	Gln	Ala	Val	Glu	Cys	Arg	Asn	Gln	Leu	Asp	
		595					600					605				
Ser	Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	
	610					615					620					
Lys	Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	
625					630					635					640	
Val	Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	
				645					650					655		
Ser	Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	
			660					665					670			

Cura 468 SEQ list 0405.txt

Ala Leu Asp Asp Ser Ala Cys Pro Gln Pro Arg Pro Pro Val Leu Glu  
675 680 685

Ala Cys His Gly Pro Thr Cys Pro Pro Glu Trp Ala Ala Leu Asp Trp  
690 695 700

Ser Glu Cys Thr Pro Ser Cys Gly Pro Gly Leu Arg His Arg Val Val  
705 710 715 720

Leu Cys Lys Ser Ala Asp His Arg Ala Thr Leu Pro Pro Ala His Cys  
725 730 735

Ser Pro Ala Ala Lys Pro Pro Ala Thr Met Arg Cys Asn Leu Arg Arg  
740 745 750

Cys Pro Pro Ala Arg Trp Val Ala Gly Glu Trp Gly Glu Cys Ser Ala  
755 760 765

Gln Cys Gly Val Gly Gln Arg Gln Arg Ser Val Arg Cys Thr Ser His  
770 775 780

Thr Gly Gln Ala Ser His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr  
785 790 795 800

Thr Gln Gln Cys Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly  
805 810 815

Pro Glu Glu Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val  
820 825 830

Leu Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys  
835 840 845

Lys Thr Cys His Gly His  
850

<210> 34

<211> 860

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (450)

<223> Wherein Xaa is any amino acid.

<400> 34

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Val	Ala	Asp	Lys	Met	Met	Val	Gly	Tyr	His	Gly	Arg	Lys	Asp	Ile	Glu	260	265	270
His	Tyr	Ile	Leu	Ser	Val	Met	Asn	Ile	Val	Ala	Lys	Leu	Tyr	Arg	Asp	275	280	285
Ser	Ser	Leu	Gly	Asn	Val	Val	Asn	Ile	Ile	Val	Ala	Arg	Leu	Ile	Val	290	295	300
Leu	Thr	Glu	Asp	Gln	Pro	Asn	Leu	Glu	Ile	Asn	His	His	Ala	Asp	Lys	305	310	315
Ser	Leu	Asp	Ser	Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Leu	Ser	His	Gln	325	330	335
Ser	Asp	Gly	Asn	Thr	Ile	Pro	Glu	Asn	Gly	Ile	Ala	His	His	Asp	Asn	340	345	350
Ala	Val	Leu	Ile	Thr	Arg	Tyr	Asp	Ile	Cys	Thr	Tyr	Lys	Asn	Lys	Pro	355	360	365
Cys	Gly	Thr	Leu	Gly	Leu	Ala	Ser	Val	Ala	Gly	Met	Cys	Glu	Pro	Glu	370	375	380
Arg	Ser	Cys	Ser	Ile	Asn	Glu	Asp	Ile	Gly	Leu	Gly	Ser	Ala	Phe	Thr	385	390	395
Ile	Ala	His	Glu	Ile	Val	His	Asn	Phe	Gly	Met	Asn	His	Asp	Gly	Ile	405	410	415
Gly	Asn	Ser	Cys	Gly	Arg	Lys	Val	Met	Lys	Gln	Gln	Asn	Tyr	Gly	Ser	420	425	430
Ser	His	Tyr	Cys	Glu	Tyr	Gln	Ser	Phe	Phe	Leu	Val	Cys	Leu	Gln	Ser	435	440	445
Arg	Xaa	His	His	Gln	Leu	Phe	Arg	Glu	Val	Cys	Arg	Glu	Leu	Trp	Cys	450	455	460
Leu	Ser	Lys	Ser	Asn	Arg	Cys	Val	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	465	470	475
Gly	Thr	Leu	Cys	Gln	Thr	Gly	Asn	Ile	Glu	Lys	Gly	Trp	Cys	Tyr	Gln	485	490	495
Gly	Asp	Cys	Val	Pro	Phe	Gly	Thr	Trp	Pro	Gln	Ser	Ile	Asp	Gly	Gly	500	505	510

Cura 468 SEQ list 0405.txt

Trp	Gly	Pro	Trp	Ser	Leu	Trp	Gly	Glu	Cys	Ser	Arg	Thr	Cys	Gly	Gly		
		515					520					525					
Gly	Val	Ser	Ser	Ser	Leu	Arg	His	Cys	Asp	Ser	Pro	Ala	Pro	Ser	Gly		
	530					535					540						
Gly	Gly	Lys	Tyr	Cys	Leu	Gly	Glu	Arg	Lys	Arg	Tyr	Arg	Ser	Cys	Asn		
545					550					555					560		
Thr	Asp	Pro	Cys	Pro	Leu	Gly	Ser	Arg	Asp	Phe	Arg	Glu	Lys	Gln	Cys		
				565					570					575			
Ala	Asp	Phe	Asp	Asn	Met	Pro	Phe	Arg	Gly	Lys	Tyr	Tyr	Asn	Trp	Lys		
			580					585					590				
Pro	Tyr	Thr	Gly	Gly	Gly	Val	Lys	Pro	Cys	Ala	Leu	Asn	Cys	Leu	Ala		
		595					600					605					
Glu	Gly	Tyr	Asn	Phe	Tyr	Thr	Glu	Arg	Ala	Pro	Ala	Val	Ile	Asp	Gly		
	610					615					620						
Thr	Gln	Cys	Asn	Ala	Asp	Ser	Leu	Asp	Ile	Cys	Ile	Asn	Gly	Glu	Cys		
625					630					635					640		
Lys	His	Val	Gly	Cys	Asp	Asn	Ile	Leu	Gly	Ser	Asp	Ala	Arg	Glu	Asp		
				645					650					655			
Arg	Cys	Arg	Val	Cys	Gly	Gly	Gly	Gly	Ser	Thr	Cys	Asp	Ala	Ile	Glu		
			660					665						670			
Gly	Phe	Phe	Asn	Asp	Ser	Leu	Pro	Arg	Gly	Gly	Tyr	Met	Glu	Val	Val		
		675					680					685					
Gln	Ile	Pro	Arg	Gly	Ser	Val	His	Ile	Glu	Val	Arg	Glu	Val	Ala	Met		
	690					695					700						
Ser	Lys	Asn	Tyr	Ile	Ala	Leu	Lys	Ser	Glu	Gly	Asp	Asp	Tyr	Tyr	Ile		
705					710					715					720		
Asn	Gly	Ala	Trp	Thr	Ile	Asp	Trp	Pro	Arg	Lys	Phe	Asp	Val	Ala	Gly		
				725					730					735			
Thr	Ala	Phe	His	Tyr	Lys	Arg	Pro	Thr	Asp	Glu	Pro	Glu	Ser	Leu	Glu		
			740					745					750				
Ala	Leu	Gly	Pro	Thr	Ser	Glu	Asn	Leu	Ile	Val	Met	Val	Leu	Leu	Gln		
		755					760					765					

Cura 468 SEQ list 0405.txt

Glu Gln Asn Leu Gly Ile Arg Tyr Lys Phe Asn Val Pro Ile Thr Arg  
770 775 780

Thr Gly Ser Gly Asp Asn Glu Val Gly Phe Thr Trp Asn His Gln Pro  
785 790 795 800

Trp Ser Glu Cys Ser Ala Thr Cys Ala Gly Gly Lys Met Pro Thr Arg  
805 810 815

Gln Pro Thr Gln Arg Ala Arg Trp Arg Thr Lys His Ile Leu Ser Tyr  
820 825 830

Ala Leu Cys Leu Leu Lys Lys Leu Ile Gly Asn Ile Ser Cys Arg Phe  
835 840 845

Ala Ser Ser Cys Asn Leu Ala Lys Glu Thr Leu Leu  
850 855 860

<210> 35

<211> 936

<212> PRT

<213> Homo sapiens

<400> 35

Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp  
1 5 10 15

Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu  
20 25 30

Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg  
35 40 45

Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln  
50 55 60

Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val  
65 70 75 80

Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu  
85 90 95

Asn Asp Gln Asp Asn Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile  
100 105 110

Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met

## Cura 468 SEQ list 0405.txt

115							120								125
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys
130						135					140				
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His
145					150					155					160
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly
				165					170					175	
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr
			180					185					190		
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val
		195					200					205			
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile
						215					220				
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu
225					230					235					240
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val
				245					250					255	
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu
			260					265					270		
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val
		275					280					285			
Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu
		290				295					300				
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp
305					310					315					320
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala
				325					330					335	
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val
			340					345					350		
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu
		355					360					365			
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro

## Cura 468 SEQ list 0405.txt

370						375						380					
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn		
385					390					395					400		
Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile		
				405					410					415			
Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr		
			420					425					430				
Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val		
		435					440					445					
Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	Pro	Glu	Ile	Lys	Ser		
	450					455					460						
Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr		
465					470					475					480		
Lys	His	Tyr	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg		
				485					490					495			
Asn	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala		
			500					505					510				
Gln	Ala	Arg	Ala	Tyr	Ile	Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala		
		515					520					525					
Leu	Ile	Trp	Leu	Ser	Gln	Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser		
	530					535					540						
Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu		
545					550					555					560		
Val	Thr	Leu	Ser	Ala	Tyr	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu		
				565					570					575			
Thr	Val	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser		
			580					585					590				
Ala	Trp	Lys	Thr	Ala	Gln	Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr		
		595					600					605					
Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys		
	610					615					620						
Arg	Lys	Glu	Val	Leu	Lys	Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp		

625				630						635				640			
Asn	Ser	Val	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly		
				645					650					655			
His	Phe	Tyr	Glu	Pro	Gln	Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser		
				660					665					670			
Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu		
				675					680					685			
Asp	Leu	Thr	Ser	Ala	Thr	Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln		
				690					695					700			
Asn	Ala	Gln	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu		
				705					710					715			
His	Ala	Leu	Ser	Lys	Tyr	Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys		
				725					730					735			
Ala	Ala	Gln	Val	Thr	Ile	Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe		
				740					745					750			
Gln	Val	Asp	Asn	Asn	Asn	Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro		
				755					760					765			
Glu	Leu	Pro	Gly	Glu	Tyr	Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val		
				770					775					780			
Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu		
				785					790					795			
Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu		
				805					810					815			
Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr		
				820					825					830			
Gly	Ser	Arg	Ser	Ala	Ser	Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val		
				835					840					845			
Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser		
				850					855					860			
Asn	His	Val	Ser	Arg	Thr	Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr		
				865					870					875			
Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu		

## Cura 468 SEQ list 0405.txt

885

890

895

Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr  
                   900                                  905                                  910

Asp Tyr Tyr Glu Thr Gly Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro  
                   915                                  920                                  925

Cys Ser Lys Asp Leu Gly Asn Ala  
           930                                  935

&lt;210&gt; 36

&lt;211&gt; 898

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp  
   1                                  5                                  10                                  15

Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu  
                   20                                  25                                  30

Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg  
           35                                  40                                  45

Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln  
   50                                  55                                  60

Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val  
   65                                  70                                  75                                  80

Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu  
                   85                                  90                                  95

Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile  
                   100                                  105                                  110

Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met  
           115                                  120                                  125

Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys  
   130                                  135                                  140

Ile Arg Lys Glu Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro  
   145                                  150                                  155                                  160

Cura 468 SEQ list 0405.txt

Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	Asn	Ser	Ala	Gly	Val	Ala	165	170	175
Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly	180	185	190
Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu	Gly	Ile	Ser	Ser	Thr	Ala	195	200	205
Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr	210	215	220
Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn	225	230	235
Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val	Gln	Leu	Glu	Ala	Ser	Pro	245	250	255
Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu	Gln	Ala	Pro	His	Cys	Ile	260	265	270
Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp	Ala	Val	Thr	Pro	Lys	Ser	275	280	285
Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Gln	290	295	300
Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val	Pro	Glu	His	Gly	Arg	Lys	305	310	315
Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu	Lys	325	330	335
Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Ser	Gly	Gly	Glu	Val	Ser	340	345	350
Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn	Val	Val	Glu	Glu	Ser	Ala	355	360	365
Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	370	375	380
Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	385	390	395
Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	Glu	405	410	415



Cura 468 SEQ list 0405.txt

Thr	Gln	Gln	Leu	Thr	Pro	Glu	Val	Lys	Ser	Lys	Ala	Ile	Gly	Tyr	Leu	420	425	430
Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Tyr	Asp	Gly	Ser	435	440	445
Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg	Asn	Gln	Gly	Asn	Thr	Trp	450	455	460
Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala	Gln	Ala	Arg	Ala	Tyr	Ile	465	470	475
Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala	Leu	Ile	Trp	Leu	Ser	Gln	485	490	495
Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu	Asn	500	505	510
Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala	Tyr	515	520	525
Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu	Thr	Val	Thr	His	Pro	Val	530	535	540
Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser	Ala	Trp	Lys	Thr	Ala	Gln	545	550	555
Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	565	570	575
Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys	Arg	Lys	Glu	Val	Leu	Lys	580	585	590
Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp	Asn	Ser	Val	His	Trp	Glu	595	600	605
Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly	His	Phe	Tyr	Glu	Pro	Gln	610	615	620
Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser	Tyr	Val	Leu	Leu	Ala	Tyr	625	630	635
Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu	Asp	Leu	Thr	Ser	Ala	Thr	645	650	655
Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln	Asn	Ala	Gln	Gly	Gly	Phe	660	665	670

Cura 468 SEQ list 0405.txt

Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	Tyr		
		675					680					685					
Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys	Ala	Ala	Gln	Val	Thr	Ile		
	690					695					700						
Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe	Gln	Val	Asp	Asn	Asn	Asn		
705					710					715					720		
Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro	Glu	Leu	Pro	Gly	Glu	Tyr		
				725					730					735			
Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser	Leu		
			740					745					750				
Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu	Phe	Pro	Phe	Ala	Leu	Gly		
		755					760					765					
Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu	Pro	Lys	Ala	His	Thr	Ser		
	770					775					780						
Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr	Gly	Ser	Arg	Ser	Ala	Ser		
785					790					795					800		
Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro	Leu		
				805					810					815			
Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	Asn	His	Val	Ser	Arg	Thr		
			820					825					830				
Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser	Asn		
		835					840					845					
Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu	Gln	Asp	Val	Pro	Val	Arg		
	850					855					860						
Asp	Leu	Lys	Pro	Ala	Ile	Val	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Thr	Asp		
865					870					875					880		
Glu	Phe	Ala	Ile	Ala	Glu	Tyr	Asn	Ala	Pro	Cys	Ser	Lys	Asp	Leu	Gly		
				885					890					895			

Asn Ala

<210> 37  
<211> 936

Cura 468 SEQ list 0405.txt

<212> PRT

<213> Homo sapiens

<400> 37

Arg	Leu	Leu	Ile	Tyr	Ala	Val	Leu	Pro	Thr	Gly	Asp	Val	Ile	Gly	Asp	1	5	10	15
Ser	Ala	Lys	Tyr	Asp	Val	Glu	Asn	Glu	Leu	Ala	Asn	Lys	Val	Asp	Leu	20	25	30	
Ser	Phe	Ser	Pro	Ser	Gln	Ser	Leu	Pro	Ala	Ser	His	Ala	His	Leu	Arg	35	40	45	
Val	Thr	Ala	Ala	Pro	Gln	Ser	Val	Cys	Ala	Leu	Arg	Ala	Val	Asp	Gln	50	55	60	
Ser	Val	Leu	Leu	Met	Lys	Pro	Asp	Ala	Glu	Leu	Ser	Ala	Ser	Ser	Val	65	70	75	80
Tyr	Asn	Leu	Leu	Pro	Glu	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Pro	Leu	85	90	95	
Asn	Asp	Gln	Asp	Asp	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile	100	105	110	
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met	115	120	125	
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys	130	135	140	
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His	145	150	155	160
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly	165	170	175	
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr	180	185	190	
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	195	200	205	
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile	210	215	220	
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu	225	230	235	240

Cura 468 SEQ list 0405.txt

Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val
				245					250					255	
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu
			260					265					270		
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val
		275					280					285			
Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu
	290					295					300				
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp
305					310					315					320
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala
				325					330					335	
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val
			340					345					350		
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu
		355					360					365			
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro
	370					375					380				
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn
385					390					395					400
Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile
				405					410					415	
Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr
			420					425					430		
Gly	Cys	Gly	Glu	Glx	Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val
		435					440					445			
Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	Pro	Glu	Ile	Lys	Ser
	450					455					460				
Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr
465					470					475					480
Lys	His	Tyr	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg
				485					490					495	

Cura 468 SEQ list 0405.txt

Asn	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala	
			500					505					510			
Gln	Ala	Arg	Ala	Tyr	Ile	Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala	
		515					520					525				
Leu	Ile	Trp	Leu	Ser	Gln	Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	
	530					535					540					
Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu	
545					550					555					560	
Val	Thr	Leu	Ser	Ala	Tyr	Ile	Lys	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu	
				565					570					575		
Thr	Val	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser	
			580					585					590			
Ala	Trp	Lys	Thr	Ala	Glu	Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr	
		595					600					605				
Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys	
	610					615					620					
Arg	Lys	Glu	Val	Leu	Lys	Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp	
625					630					635					640	
Asn	Ser	Val	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly	
				645					650					655		
His	Phe	Tyr	Glu	Pro	Gln	Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser	
			660					665					670			
Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu	
		675					680					685				
Asp	Leu	Thr	Ser	Ala	Thr	Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln	
	690					695					700					
Asn	Ala	Gln	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Lys	Val	Val	Ala	Leu	
705					710					715					720	
His	Ala	Leu	Ser	Lys	Tyr	Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys	
				725					730					735		
Ala	Ala	Gln	Val	Thr	Ile	Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe	
			740					745					750			

Cura 468 SEQ list 0405.txt

Gln	Val	Asp	Asn	Asn	Asn	Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro	
		755					760					765				
Glu	Leu	Pro	Gly	Glu	Tyr	Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	
	770					775					780					
Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu	
785					790					795					800	
Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu	
				805					810					815		
Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr	
			820					825					830			
Gly	Ser	Arg	Ser	Ala	Ser	Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val	
		835					840					845				
Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	
	850					855					860					
Asn	His	Val	Ser	Arg	Thr	Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr	
865					870					875					880	
Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu	
				885					890					895		
Gln	Asp	Val	Pro	Val	Arg	Asp	Leu	Lys	Pro	Ala	Ile	Val	Lys	Val	Tyr	
			900					905					910			
Asp	Tyr	Tyr	Glu	Thr	Asp	Glu	Phe	Ala	Ile	Ala	Glu	Tyr	Asn	Ala	Pro	
	915						920					925				
Cys	Ser	Lys	Asp	Leu	Gly	Asn	Ala									
	930					935										

<210> 38

<211> 931

<212> PRT

<213> Rattus norvegicus

<400> 38

Arg	Leu	Val	Leu	Tyr	Ala	Ile	Leu	Pro	Asn	Gly	Glu	Val	Val	Gly	Asp	
1				5					10					15		

Thr Ala Lys Tyr Glu Ile Glu Asn Cys Leu Ala Asn Lys Val Asp Leu

Cura 468 SEQ list 0405.txt

20

25

30

Val	Phe	Arg	Pro	Asn	Ser	Gly	Leu	Pro	Ala	Thr	Arg	Ala	Leu	Leu	Ser
		35					40					45			
Val	Met	Ala	Ser	Pro	Gln	Ser	Leu	Cys	Gly	Leu	Arg	Ala	Val	Asp	Gln
	50					55					60				
Ser	Val	Leu	Leu	Met	Lys	Pro	Glu	Thr	Glu	Leu	Ser	Ala	Ser	Leu	Ile
65					70					75					80
Tyr	Asp	Leu	Leu	Pro	Val	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gln	Gly	Ala
				85					90					95	
Asp	Gln	Arg	Glu	Glu	Asp	Thr	Asn	Gly	Cys	Val	Lys	Gln	Asn	Asp	Thr
			100					105					110		
Tyr	Ile	Asn	Gly	Ile	Leu	Tyr	Ser	Pro	Val	Gln	Asn	Thr	Asn	Glu	Glu
	115						120					125			
Asp	Met	Tyr	Gly	Phe	Leu	Lys	Asp	Met	Gly	Leu	Lys	Val	Phe	Thr	Asn
	130					135					140				
Ser	Asn	Ile	Arg	Lys	Pro	Lys	Val	Cys	Glu	Arg	Leu	Arg	Asp	Asn	Lys
145					150					155					160
Gly	Ile	Pro	Ala	Ala	Tyr	His	Leu	Val	Ser	Gln	Ser	His	Met	Asp	Ala
				165					170					175	
Phe	Leu	Glu	Ser	Ser	Glu	Ser	Pro	Thr	Glu	Thr	Arg	Arg	Ser	Tyr	Phe
			180					185					190		
Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	Asp	Ser	Ala	Gly	Val
		195					200					205			
Ala	Glu	Val	Glu	Val	Thr	Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala
	210					215					220				
Gly	Ala	Phe	Cys	Leu	Ser	Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Val
225					230					235					240
Val	Gln	Phe	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro
				245					250					255	
Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu
			260					265					270		
Asn	Tyr	Leu	Pro	Thr	Cys	Ile	Arg	Val	Ala	Val	Gln	Leu	Glu	Ala	Ser

## Cura 468 SEQ list 0405.txt

275							280									285
Pro	Asp	Phe	Leu	Ala	Ala	Pro	Glu	Glu	Lys	Glu	Gln	Arg	Ser	His	Cys	
290						295					300					
Ile	Cys	Met	Asn	Gln	Arg	His	Thr	Ala	Ser	Trp	Ala	Val	Ile	Pro	Lys	
305					310					315					320	
Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Asn	Ser	
			325						330					335		
Lys	Glu	Leu	Cys	Gly	Asn	Glu	Val	Pro	Val	Val	Pro	Glu	Gln	Gly	Lys	
			340					345					350			
Lys	Asp	Thr	Ile	Ile	Lys	Ser	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu	
	355						360					365				
Asn	Glu	Val	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Met	Gly	Ala	Glu	Val	
	370					375					380					
Ser	Glu	Leu	Ile	Ala	Leu	Lys	Leu	Pro	Ser	Asp	Val	Val	Glu	Glu	Ser	
385					390					395					400	
Ala	Arg	Ala	Ser	Val	Thr	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	
				405					410					415		
Gln	Asn	Thr	Gln	Asp	Leu	Leu	Lys	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	
			420					425					430			
Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	
	435						440					445				
Glu	Thr	Gln	Gln	Leu	Thr	Gln	Glu	Ile	Lys	Thr	Lys	Ala	Ile	Ala	Tyr	
	450					455					460					
Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Arg	Asp	Gly	
465					470					475					480	
Ser	Tyr	Ser	Ala	Phe	Gly	Asp	Lys	Pro	Gly	Arg	Asn	His	Ala	Asn	Thr	
				485					490					495		
Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Lys	Tyr	
			500					505					510			
Ile	Phe	Ile	Asp	Glu	Val	His	Ile	Thr	Gln	Ala	Leu	Leu	Trp	Leu	Ser	
	515						520					525				
Gln	Gln	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu	



Cura 468 SEQ list 0405.txt

530																	
Asn	Asn	Ala	Met	Lys	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala		
545					550					555					560		
Tyr	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Met	Ser	Leu	Pro	Val	Thr	His	Pro		
				565					570					575			
Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala		
			580					585					590				
Arg	Gly	Gly	Ala	Gly	Gly	Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala		
		595					600					605					
Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys		
	610					615					620						
Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala	Arg	Gly	Gly	Ala	Gly	Gly	Ser	His		
625					630					635					640		
Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro		
				645					650					655			
Gln	Ala	Thr	Ser	Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Val	Leu	Leu	Ala		
			660					665					670				
Tyr	Leu	Thr	Thr	Glu	Pro	Ala	Pro	Thr	Gln	Glu	Asp	Leu	Thr	Ala	Ala		
		675					680					685					
Met	Leu	Ile	Val	Lys	Trp	Leu	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly		
	690					695					700						
Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys		
705					710					715					720		
Tyr	Gly	Ser	Ala	Thr	Phe	Thr	Arg	Ala	Lys	Lys	Ala	Ala	Gln	Val	Thr		
				725					730					735			
Ile	Arg	Ser	Ser	Gly	Thr	Phe	Ser	Thr	Lys	Phe	Gln	Val	Asn	Asn	Asn		
			740					745					750				
Asn	Gln	Leu	Leu	Leu	Gln	Arg	Val	Thr	Leu	Pro	Thr	Val	Pro	Gly	Asp		
		755					760					765					
Tyr	Thr	Val	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser		
	770					775					780						
Leu	Lys	Tyr	Ser	Val	Leu	Pro	Arg	Glu	Glu	Glu	Phe	Pro	Phe	Ala	Val		

Cura 468 SEQ list 0405.txt

785 790 795 800

Val Val Gln Thr Leu Pro Gly Thr Cys Glu Asp Pro Lys Ala His Thr  
805 810 815

Ser Phe Gln Ile Ser Leu Asn Ile Ser Tyr Thr Gly Ser Arg Ser Glu  
820 825 830

Ser Asn Met Ala Ile Ala Asp Val Lys Met Val Ser Gly Phe Ile Pro  
835 840 845

Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Val His Val Ser Arg  
850 855 860

Thr Glu Val Ser Asn Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser  
865 870 875 880

Asn Gln Thr Val Asn Leu Ser Phe Thr Val Gln Gln Asp Ile Pro Ile  
885 890 895

Arg Asp Leu Lys Pro Ala Val Val Lys Val Tyr Asp Tyr Tyr Glu Lys  
900 905 910

Asp Glu Phe Ala Val Ala Lys Tyr Ser Ala Pro Cys Ser Thr Asp Tyr  
915 920 925

Gly Asn Ala  
930

<210> 39

<211> 941

<212> PRT

<213> Cavia porcellus

<400> 39

Arg Val Leu Ile Tyr Ala Ile Leu Pro Ser Gly Glu Ile Ile Ala Asp  
1 5 10 15

Ser Ala Lys Tyr Asn Val Glu Asn Cys Leu Asp Asn Lys Val Asn Leu  
20 25 30

Ser Phe Ser Glu Gly Gln Ser Leu Pro Ala Ser Lys Thr His Leu Arg  
35 40 45

Val Thr Ala Ser Pro Gln Ser Leu Cys Ala Leu Arg Ala Val Asp Gln  
50 55 60

Cura 468 SEQ list 0405.txt

Ser	Val	Leu	Leu	Arg	Lys	Pro	Glu	Ala	Val	Leu	Ser	Ala	Ser	Ser	Val	65	70	75	80
Tyr	Ala	Leu	Leu	Pro	Val	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Leu	Leu	85	90	95	
Gly	Gln	Gln	Glu	Glu	Asn	Asp	Gly	Glu	Cys	Val	Ser	Leu	Tyr	Asn	Thr	100	105	110	
Tyr	Ile	Asp	Gly	Ile	Leu	Tyr	Ser	Pro	Glu	Pro	Asn	Ile	Asn	Glu	Lys	115	120	125	
Asp	Met	Tyr	Gly	Phe	Leu	Lys	Asp	Met	Gly	Leu	Lys	Val	Phe	Thr	Asn	130	135	140	
Thr	Lys	Ile	Gln	Lys	Pro	Gln	Leu	Cys	Ala	His	Val	Gln	Lys	Phe	Glu	145	150	155	160
Val	Pro	Thr	Met	Ala	Tyr	Ser	Tyr	Ser	Glu	Ser	Ser	Ser	Phe	Arg	Ser	165	170	175	
Gly	Pro	Arg	Arg	Val	Pro	Ala	Val	Gly	Ile	Ala	Ala	Thr	Tyr	Ser	Glu	180	185	190	
Pro	Pro	Lys	Glu	Thr	Val	Arg	Thr	Tyr	Ser	Pro	Glu	Thr	Trp	Ile	Trp	195	200	205	
Asp	Leu	Lys	Val	Thr	Asp	Ser	Ser	Gly	Val	Ala	Glu	Val	Glu	Val	Thr	210	215	220	
Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	225	230	235	240
Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Thr	Ala	Ser	Leu	Arg	Ala	Phe	245	250	255	
Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	260	265	270	
Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Asp	Cys	275	280	285	
Ile	Arg	Ile	Ser	Val	His	Leu	Glu	Ala	Ser	Pro	Lys	Phe	Leu	Ala	Glu	290	295	300	
Pro	Lys	Ala	Lys	Glu	Gln	Glu	Ser	Tyr	Cys	Val	Cys	Gly	Asn	Glu	Arg	305	310	315	320

Cura 468 SEQ list 0405.txt

Gln	Thr	Val	Ser	Trp	Val	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn
				325					330					335	
Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Ser	Glu	Leu	Cys	Gly	Asn
			340					345					350		
Glu	Lys	Thr	Val	Val	Pro	Thr	Tyr	Gly	Lys	Lys	Asp	Thr	Ile	Ile	Lys
		355					360					365			
Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Ile	Glu	Lys	Glu	Glu	Thr	Trp	Thr
	370					375					380				
Ser	Leu	Ile	Arg	Val	Ser	Asp	Thr	Thr	Val	Ser	Glu	Lys	Leu	His	Leu
385					390					395					400
Glu	Leu	Pro	Ser	Asn	Val	Ile	Gln	Asp	Ser	Ala	Arg	Ala	Thr	Val	Ser
				405					410					415	
Ile	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	Asn	Ile	Gln	Asn	Leu
			420					425					430		
Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	Ala
		435					440					445			
Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr
	450					455					460				
Pro	Asp	Ile	Lys	Ser	Lys	Ala	Ile	Ser	Tyr	Leu	Ser	Thr	Gly	Tyr	Gln
465					470					475					480
Arg	Gln	Leu	Asn	Tyr	Lys	His	Arg	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly
				485					490					495	
Glu	Asn	Tyr	Arg	Gly	Gly	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val
			500					505					510		
Leu	Lys	Thr	Phe	Ser	Gln	Ala	Arg	Lys	Tyr	Ile	Phe	Ile	Asp	Glu	Ala
		515					520					525			
His	Ile	Thr	Gln	Ala	Leu	Ser	Trp	Leu	Ser	Gln	Lys	Gln	Lys	Asp	Asn
	530					535					540				
Gly	Cys	Phe	Trp	Ser	Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly
545					550					555					560
Gly	Val	Glu	Asp	Glu	Ile	Ser	Leu	Ser	Ala	Tyr	Ile	Thr	Ile	Ala	Leu
				565					570					575	

Cura 468 SEQ list 0405.txt

Leu	Glu	Met	Ser	Leu	Pro	Asp	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	
			580					585					590			
Phe	Cys	Leu	Glu	Ser	Ala	Trp	Lys	Ser	Ala	Lys	Glu	Gly	Thr	His	Gly	
		595					600					605				
Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	
	610					615					620					
Gly	Asn	Gln	Glu	Arg	Lys	Lys	Glu	Ile	Leu	Lys	Ser	Leu	Glu	Asp	Glu	
625					630					635					640	
Gly	Val	Lys	Glu	Asp	Asn	Ser	Leu	His	Trp	Ala	Arg	Pro	Gln	Lys	Pro	
				645					650					655		
Lys	Val	Ser	Glu	Gly	Phe	Leu	Phe	Lys	Ser	Gln	Ala	Pro	Ser	Ala	Glu	
			660					665						670		
Val	Glu	Met	Thr	Ser	Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Arg	Pro	
		675					680					685				
Ala	Pro	Thr	Pro	Glu	Asp	Leu	Thr	Ser	Ala	Thr	Asp	Ile	Val	Asn	Trp	
		690				695					700					
Val	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly	Tyr	Ser	Ser	Thr	Gln	Asp	
705					710					715					720	
Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	Tyr	Ala	Ala	Ala	Thr	Phe	
				725					730					735		
Thr	Arg	Thr	Glu	Lys	Ala	Ala	Gln	Val	Thr	Ile	Lys	Ser	Ser	Gly	Thr	
			740					745						750		
Phe	Ser	Thr	Asn	Phe	Glu	Val	Asn	His	Asn	Asn	Arg	Leu	Leu	Leu	Gln	
		755					760					765				
Gln	Val	Ser	Leu	Pro	Thr	Val	Ser	Asp	Ser	Tyr	Thr	Ile	Thr	Val	Thr	
						775					780					
Gly	Glu	Gly	Asn	Val	Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Val	Pro	
785					790					795					800	
Ser	Glu	Lys	Gly	Thr	Phe	Pro	Phe	Ala	Leu	Glu	Ala	Glu	Thr	Val	Pro	
				805					810					815		
Gln	Ala	Cys	Asp	Gly	Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	
			820					825					830			

Cura 468 SEQ list 0405.txt

Asn	Val	Ser	Tyr	Ile	Gly	Ser	Arg	Pro	Val	Ser	Asn	Met	Ala	Ile	Val
		835					840					845			
Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys
		850				855					860				
Asn	Leu	Glu	Lys	Ser	Glu	His	Ile	Ser	Arg	Thr	Glu	Val	Ser	Asn	Asn
865					870					875					880
His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu
				885					890					895	
Ser	Phe	Phe	Val	Val	Gln	Asp	Ile	Glu	Val	Arg	Asp	Leu	Lys	Pro	Ala
			900					905					910		
Ile	Ile	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Thr	Asn	Glu	Phe	Ala	Ile	Ala
		915					920					925			
Glu	Tyr	His	Ala	Pro	Cys	Ser	Lys	Asp	Pro	Gly	Asn	Ala			
	930					935					940				

<210> 40  
 <211> 373  
 <212> PRT  
 <213> Mus musculus

<400> 40	
Met Ser Thr Asp Cys Ala Gly Asn Ser Thr Cys Pro Val Asn Ser Thr	
1 5 10 15	
Glu Glu Asp Pro Pro Val Gly Met Glu Gly His Ala Asn Leu Lys Leu	
20 25 30	
Leu Phe Thr Val Leu Ser Ala Val Met Val Gly Leu Val Met Phe Ser	
35 40 45	
Phe Gly Cys Ser Val Glu Ser Gln Lys Leu Trp Leu His Leu Arg Arg	
50 55 60	
Pro Trp Gly Ile Ala Val Gly Leu Leu Ser Gln Phe Gly Leu Met Pro	
65 70 75 80	
Leu Thr Ala Tyr Leu Leu Ala Ile Gly Phe Gly Leu Lys Pro Phe Gln	
85 90 95	
Ala Ile Ala Val Leu Met Met Gly Ser Cys Pro Gly Gly Thr Ile Ser	
100 105 110	

Cura 468 SEQ list 0405.txt

Asn	Val	Leu	Thr	Phe	Trp	Val	Asp	Gly	Asp	Met	Asp	Leu	Ser	Ile	Ser		
		115					120					125					
Met	Thr	Thr	Cys	Ser	Thr	Val	Ala	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys		
	130					135					140						
Leu	Tyr	Ile	Tyr	Thr	Arg	Ser	Trp	Thr	Leu	Thr	Gln	Asn	Leu	Val	Ile		
145					150					155					160		
Pro	Tyr	Gln	Ser	Ile	Gly	Ile	Thr	Leu	Val	Ser	Leu	Val	Val	Pro	Val		
				165					170					175			
Ala	Ser	Gly	Val	Tyr	Val	Asn	Tyr	Arg	Trp	Pro	Lys	Gln	Ala	Thr	Val		
			180					185					190				
Ile	Leu	Lys	Val	Gly	Ala	Ile	Leu	Gly	Gly	Met	Leu	Leu	Leu	Val	Val		
		195					200					205					
Ala	Val	Thr	Gly	Met	Val	Leu	Ala	Lys	Gly	Trp	Asn	Thr	Asp	Val	Thr		
	210					215					220						
Leu	Leu	Val	Ile	Ser	Cys	Ile	Phe	Pro	Leu	Val	Gly	His	Val	Thr	Gly		
225					230					235					240		
Phe	Leu	Leu	Ala	Phe	Leu	Thr	His	Gln	Ser	Trp	Gln	Arg	Cys	Arg	Thr		
				245					250					255			
Ile	Ser	Ile	Glu	Thr	Gly	Ala	Gln	Asn	Ile	Gln	Leu	Cys	Ile	Ala	Met		
			260					265					270				
Leu	Gln	Leu	Ser	Phe	Ser	Ala	Glu	Tyr	Leu	Val	Gln	Leu	Leu	Asn	Phe		
		275					280					285					
Ala	Leu	Ala	Tyr	Gly	Leu	Phe	Gln	Val	Leu	His	Gly	Leu	Leu	Ile	Val		
	290					295					300						
Ala	Ala	Tyr	Gln	Ala	Tyr	Lys	Arg	Arg	Gln	Lys	Ser	Lys	Cys	Arg	Arg		
305					310					315					320		
Gln	His	Pro	Asp	Cys	Pro	Asp	Val	Cys	Tyr	Glu	Lys	Gln	Pro	Arg	Glu		
				325					330					335			
Thr	Ser	Ala	Phe	Leu	Asp	Lys	Gly	Asp	Glu	Ala	Ala	Val	Thr	Leu	Gly		
			340					345					350				
Pro	Val	Gln	Pro	Glu	Gln	His	His	Arg	Ala	Ala	Glu	Leu	Thr	Ser	His		
		355					360					365					

Cura 468 SEQ list 0405.txt

Ile Pro Ser Cys Glu  
370

<210> 41

<211> 347

<212> PRT

<213> Orycctolagus cuniculus

<400> 41

Met	Ser	Asn	Leu	Thr	Val	Gly	Cys	Leu	Ala	Asn	Ala	Thr	Val	Cys	Glu
1				5					10					15	

Gly	Ala	Ser	Cys	Val	Ala	Pro	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Ser
			20					25					30		

Val	Val	Leu	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Leu	Val	Met	Phe
		35					40					45			

Ser	Met	Gly	Cys	Asn	Val	Glu	Ile	Lys	Lys	Phe	Leu	Gly	His	Ile	Arg
	50					55					60				

Arg	Pro	Trp	Gly	Ile	Phe	Ile	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met
65					70					75					80

Pro	Leu	Thr	Gly	Phe	Val	Leu	Ala	Val	Ala	Phe	Gly	Ile	Met	Pro	Ile
				85					90					95	

Gln	Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Ala
			100					105					110		

Ser	Asn	Ile	Leu	Ala	Tyr	Trp	Val	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val
		115					120					125			

Ser	Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu
	130					135					140				

Cys	Leu	Tyr	Val	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val
145					150					155					160

Ile	Pro	Tyr	Asp	Asn	Ile	Gly	Thr	Ser	Leu	Val	Ala	Leu	Val	Val	Pro
				165					170					175	

Val	Ser	Ile	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys
			180					185					190		

Ile	Ile	Leu	Lys	Val	Gly	Ser	Ile	Ala	Gly	Ala	Val	Leu	Ile	Val	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



Cura 468 SEQ list 0405.txt

195		200		205											
Ile	Ala	Val	Val	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu
210						215					220				
Pro	Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Met	Ala	Gly	Tyr	Ser
225					230					235					240
Leu	Gly	Phe	Phe	Leu	Ala	Arg	Ile	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys
				245					250					255	
Arg	Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser
			260					265					270		
Thr	Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Thr	Tyr	Val	Phe
		275					280					285			
Thr	Phe	Pro	Leu	Ile	Tyr	Ser	Ile	Phe	Gln	Ile	Ala	Phe	Ala	Ala	Ile
	290					295					300				
Phe	Leu	Gly	Ile	Tyr	Val	Ala	Tyr	Arg	Lys	Cys	His	Gly	Lys	Asn	Asp
305					310					315					320
Ala	Glu	Phe	Pro	Asp	Ile	Lys	Asp	Thr	Lys	Thr	Glu	Pro	Glu	Ser	Ser
				325					330					335	
Phe	His	Gln	Met	Asn	Gly	Gly	Phe	Gln	Pro	Glu					
			340					345							

<210> 42  
 <211> 348  
 <212> PRT  
 <213> Rattus norvegicus

<400> 42

Met	Asp	Asn	Ser	Ser	Val	Cys	Ser	Pro	Asn	Ala	Thr	Phe	Cys	Glu	Gly
1				5					10					15	
Asp	Ser	Cys	Leu	Val	Thr	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Ser	Thr
			20					25					30		
Val	Met	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Met	Val	Met	Phe	Ser
	35						40					45			
Met	Gly	Cys	Asn	Val	Glu	Ile	Asn	Lys	Phe	Leu	Gly	His	Ile	Lys	Arg
	50					55					60				

Cura 468 SEQ list 0405.txt

Pro	Trp	Gly	Ile	Phe	Val	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met	Pro	65	70	75	80
Leu	Thr	Gly	Phe	Ile	Leu	Ser	Val	Ala	Ser	Gly	Ile	Leu	Pro	Val	Gln		85	90	95
Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Gly	Ser		100	105	110
Asn	Ile	Leu	Ala	Tyr	Trp	Ile	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val	Ser	115	120	125	
Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys	130	135	140	
Leu	Phe	Ile	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val	Ile	145	150	155	160
Pro	Tyr	Asp	Ser	Ile	Gly	Ile	Ser	Leu	Val	Ala	Leu	Val	Ile	Pro	Val		165	170	175
Ser	Ile	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile	180	185	190	
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Ala	Gly	Ala	Ile	Leu	Ile	Val	Leu	Ile	195	200	205	
Ala	Val	Val	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu	Pro	210	215	220	
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ala	Gly	Tyr	Ser	Leu	225	230	235	240
Gly	Phe	Phe	Leu	Ala	Arg	Leu	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg		245	250	255
Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr		260	265	270
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr	275	280	285	
Phe	Pro	Leu	Ile	Tyr	Thr	Val	Phe	Gln	Leu	Val	Phe	Ala	Ala	Ile	Ile	290	295	300	
Leu	Gly	Met	Tyr	Val	Thr	Tyr	Lys	Lys	Cys	His	Gly	Lys	Asn	Asp	Ala	305	310	315	320

Cura 468 SEQ list 0405.txt

Glu Phe Leu Glu Lys Thr Asp Asn Asp Met Asp Pro Met Pro Ser Phe  
 325 330 335

Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys  
 340 345

<210> 43

<211> 348

<212> PRT

<213> Mus musculus

<400> 43

Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly  
 1 5 10 15

Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr  
 20 25 30

Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser  
 35 40 45

Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg  
 50 55 60

Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro  
 65 70 75 80

Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln  
 85 90 95

Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser  
 100 105 110

Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser  
 115 120 125

Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys  
 130 135 140

Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile  
 145 150 155 160

Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val  
 165 170 175

Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile  
 180 185 190

## Cura 468 SEQ list 0405.txt

Ile	Leu	Lys	Ile	Gly	Ser	Ile	Thr	Gly	Val	Ile	Leu	Ile	Val	Leu	Ile
		195					200					205			
Ala	Val	Ile	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu	Pro
		210				215					220				
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ala	Gly	Tyr	Ser	Leu
225					230					235					240
Gly	Phe	Phe	Leu	Ala	Arg	Leu	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg
				245					250					255	
Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr
			260					265					270		
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr
		275					280					285			
Phe	Pro	Leu	Ile	Tyr	Thr	Val	Phe	Gln	Leu	Val	Phe	Ala	Ala	Val	Ile
		290				295					300				
Leu	Gly	Ile	Tyr	Val	Thr	Tyr	Arg	Lys	Cys	Tyr	Gly	Lys	Asn	Asp	Ala
305					310					315					320
Glu	Phe	Leu	Glu	Lys	Thr	Asp	Asn	Glu	Met	Asp	Ser	Arg	Pro	Ser	Phe
				325					330					335	
Asp	Glu	Thr	Asn	Lys	Gly	Phe	Gln	Pro	Asp	Glu	Lys				
			340					345							

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<210> 44
<211> 348
<212> PRT
<213> Mus musculus
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<400> 44

Met	Asp	Asn	Ser	Ser	Val	Cys	Pro	Pro	Asn	Ala	Thr	Val	Cys	Glu	Gly
1				5					10					15	
Asp	Ser	Cys	Val	Val	Pro	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Asn	Thr
			20					25					30		
Val	Met	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Met	Val	Met	Phe	Ser
		35					40					45			
Met	Gly	Cys	Asn	Val	Glu	Val	His	Lys	Phe	Leu	Gly	His	Ile	Lys	Arg

## Cura 468 SEQ list 0405.txt

50						55						60			
Pro	Trp	Gly	Ile	Phe	Val	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met	Pro
65					70					75					80
Leu	Thr	Gly	Phe	Ile	Leu	Ser	Val	Ala	Ser	Gly	Ile	Leu	Pro	Val	Gln
				85					90					95	
Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Gly	Ser
			100					105					110		
Asn	Ile	Leu	Ala	Tyr	Trp	Ile	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val	Ser
		115					120					125			
Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys
	130					135					140				
Leu	Phe	Val	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val	Ile
145					150					155					160
Pro	Tyr	Asp	Ser	Ile	Gly	Ile	Ser	Leu	Val	Ala	Leu	Val	Ile	Pro	Val
				165					170					175	
Ser	Phe	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile
			180					185					190		
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Thr	Gly	Val	Ile	Leu	Ile	Val	Leu	Ile
		195					200					205			
Ala	Val	Ile	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu	Pro
		210				215					220				
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ala	Gly	Tyr	Ser	Leu
225					230					235					240
Gly	Phe	Phe	Leu	Ala	Arg	Leu	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg
				245					250					255	
Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr
			260					265					270		
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr
		275					280					285			
Phe	Pro	Leu	Ile	Tyr	Thr	Val	Phe	Gln	Leu	Val	Phe	Ala	Ala	Val	Ile
	290					295					300				
Leu	Gly	Ile	Tyr	Val	Thr	Tyr	Arg	Lys	Cys	Tyr	Gly	Lys	Asn	Asp	Ala

Cura 468 SEQ list 0405.txt

305 310 315 320

Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe  
325 330 335

Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys  
340 345

<210> 45  
<211> 348  
<212> PRT  
<213> Homo sapiens

<400> 45  
Met Asp Asn Ser Ser Ile Cys Asn Pro Asn Ala Thr Ile Cys Glu Gly  
1 5 10 15

Asp Ser Cys Ile Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser Val  
20 25 30

Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe Ser  
35 40 45

Met Gly Cys Asn Val Glu Leu His Lys Phe Leu Gly His Leu Arg Arg  
50 55 60

Pro Trp Gly Ile Val Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro  
65 70 75 80

Leu Thr Gly Phe Val Leu Ser Val Ala Phe Gly Ile Leu Pro Val Gln  
85 90 95

Ala Val Val Val Leu Ile Gln Gly Cys Cys Pro Gly Gly Thr Ala Ser  
100 105 110

Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val Ser  
115 120 125

Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys  
130 135 140

Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile  
145 150 155 160

Pro Tyr Asp Ser Ile Gly Thr Ser Leu Val Ala Leu Val Ile Pro Val  
165 170 175

Cura 468 SEQ list 0405.txt

Ser	Ile	Gly	Met	Tyr	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile	180	185	190
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Ala	Gly	Ala	Ile	Leu	Ile	Val	Leu	Ile	195	200	205
Ala	Val	Val	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Thr	Ile	Glu	Pro	210	215	220
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Tyr	Pro	Ile	Ala	Gly	Tyr	Gly	Leu	225	230	235
Gly	Phe	Phe	Leu	Ala	Arg	Ile	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg	245	250	255
Thr	Val	Ala	Leu	Glu	Thr	Gly	Leu	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr	260	265	270
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr	275	280	285
Phe	Pro	Leu	Ile	Tyr	Ser	Ile	Phe	Gln	Ile	Ala	Phe	Ala	Ala	Ile	Leu	290	295	300
Leu	Gly	Ala	Tyr	Val	Ala	Tyr	Lys	Lys	Cys	His	Gly	Lys	Asn	Asn	Thr	305	310	315
Glu	Leu	Gln	Glu	Lys	Thr	Asp	Asn	Glu	Met	Glu	Pro	Arg	Ser	Ser	Phe	325	330	335
Gln	Glu	Thr	Asn	Lys	Gly	Phe	Gln	Pro	Asp	Glu	Lys					340	345	

<210> 46  
 <211> 272  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu  
 1 5 10 15  
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala  
 20 25 30  
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile  
 35 40 45

Cura 468 SEQ list 0405.txt

Val	Val	Gly	Glu	Gly	Thr	His	Phe	Leu	Ile	Pro	Trp	Val	Gln	Lys	Pro
50						55					60				
Ile	Ile	Phe	Asp	Cys	Arg	Ser	Arg	Pro	Arg	Asn	Val	Pro	Val	Ile	Thr
65					70					75					80
Gly	Ser	Lys	Asp	Leu	Gln	Asn	Val	Asn	Ile	Thr	Leu	Arg	Ile	Leu	Phe
				85					90					95	
Arg	Pro	Val	Ala	Ser	Gln	Leu	Pro	Arg	Ile	Phe	Thr	Ser	Ile	Gly	Glu
			100					105					110		
Asp	Tyr	Asp	Glu	Arg	Val	Leu	Pro	Ser	Ile	Thr	Thr	Glu	Ile	Leu	Lys
		115					120					125			
Ser	Val	Val	Ala	Arg	Phe	Asp	Ala	Gly	Glu	Leu	Ile	Thr	Gln	Arg	Glu
	130					135					140				
Leu	Val	Ser	Arg	Gln	Val	Ser	Asp	Asp	Leu	Thr	Glu	Arg	Ala	Ala	Thr
145					150					155					160
Phe	Gly	Leu	Ile	Leu	Asp	Asp	Val	Ser	Leu	Thr	His	Leu	Thr	Phe	Gly
				165					170					175	
Lys	Glu	Phe	Thr	Glu	Ala	Val	Glu	Ala	Lys	Gln	Val	Ala	Gln	Gln	Glu
			180					185					190		
Ala	Glu	Arg	Ala	Arg	Phe	Val	Val	Glu	Lys	Ala	Glu	Gln	Gln	Lys	Lys
		195					200					205			
Ala	Ala	Ile	Ile	Ser	Ala	Glu	Gly	Asp	Ser	Lys	Ala	Ala	Glu	Leu	Ile
	210					215					220				
Ala	Asn	Ser	Leu	Ala	Thr	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu	Arg	Lys
225					230					235					240
Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ala	Tyr	Gln	Leu	Ser	Arg	Ser	Arg	Asn
				245					250					255	
Ile	Thr	Tyr	Leu	Pro	Ala	Gly	Gln	Ser	Val	Leu	Leu	Gln	Leu	Pro	Gln
			260					265					270		

<210> 47



Cura 468 SEQ list 0405.txt

<211> 272

<212> PRT

<213> Rattus norvegicus

<400> 47

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Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
  1              5              10              15

Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
          20              25              30

Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
          35              40              45

Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
  50              55              60

Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
  65              70              75              80

Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
          85              90              95

Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Tyr Thr Ser Ile Gly Glu
          100              105              110

Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
          115              120              125

Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
          130              135              140

Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
          145              150              155              160

Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
          165              170              175

Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
          180              185              190

Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
          195              200              205

Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile
          210              215              220

Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys

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Cura 468 SEQ list 0405.txt

225		230		235		240									
Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ala	Tyr	Gln	Leu	Ser	Arg	Ser	Arg	Asn
				245					250					255	
Ile	Thr	Tyr	Leu	Pro	Ala	Gly	Gln	Ser	Val	Leu	Leu	Gln	Leu	Pro	Gln
			260					265					270		

<210> 48  
 <211> 1798  
 <212> PRT  
 <213> Drosophila melanogaster

<400> 48

Met	Glu	Met	Arg	Glu	Val	Leu	Ser	Arg	Glu	Gly	Arg	Glu	Ala	Lys	Asn
1				5					10					15	
Leu	Leu	Val	Tyr	Gln	Phe	Cys	Asp	Glu	Thr	Thr	Ser	Ser	Gly	Ala	Thr
			20					25					30		
Ser	Gly	Phe	Gly	Ser	Thr	Gly	Gly	Asp	Val	Gly	Gly	Gly	Ser	Gly	Gly
		35					40					45			
Asp	Gly	Pro	Ala	Val	Gly	Ser	Gly	Gly	Val	Leu	Leu	Asn	Gly	Asp	Cys
	50					55						60			
Tyr	Arg	Lys	Pro	Pro	Met	Val	Pro	Pro	Lys	Ser	Pro	Asn	Gly	Thr	Pro
65					70					75					80
Lys	Asn	Cys	Gln	Ser	Pro	Thr	Ser	Pro	Arg	Leu	Lys	Ser	Ser	Ala	Ser
				85					90					95	
Val	Gly	Cys	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Pro	Arg	Val	Arg	Ser	Ala
			100					105					110		
Ser	Thr	Gly	Arg	Asp	Lys	Lys	Ser	Glu	Leu	Gln	Ala	Arg	Tyr	Trp	Ala
		115					120					125			
Leu	Leu	Phe	Gly	Asn	Leu	Gln	Arg	Ala	Ile	Asn	Glu	Ile	Tyr	Gln	Thr
	130					135					140				
Val	Glu	Cys	Tyr	Glu	Asn	Ile	Ser	Ser	Cys	Gln	Glu	Thr	Ile	Leu	Val
145					150					155					160

Cura 468 SEQ list 0405.txt

Leu	Glu	Asn	Tyr	Val	Arg	Asp	Phe	Lys	Ala	Leu	Cys	Glu	Trp	Phe	Lys	165	170	175
Val	Ser	Trp	Asp	Tyr	Glu	Ser	Arg	Pro	Leu	Gln	Gln	Arg	Pro	Gln	Ser	180	185	190
Leu	Ala	Trp	Glu	Val	Arg	Lys	Ser	Asn	Pro	Thr	Pro	Arg	Val	Arg	Thr	195	200	205
Arg	Ser	Leu	Cys	Ser	Pro	Asn	Asn	Ser	Gly	Lys	Ser	Ser	Pro	Ala	Leu	210	215	220
Phe	Pro	Gly	Thr	Gln	Ser	Gly	Glu	Thr	Ser	Pro	Phe	Cys	Asp	Asn	Gly	225	230	235
Gln	Ile	Ser	Pro	Arg	Lys	Leu	Leu	Arg	Ala	Tyr	Asp	Gln	Val	Pro	Lys	245	250	255
Gly	Ala	Met	Arg	Leu	Asn	Val	Arg	Glu	Leu	Phe	Ala	Ala	Ser	Lys	Arg	260	265	270
Ala	Thr	Gln	Gly	Ser	Ser	Gln	Ser	Asp	Asn	Met	Glu	Gly	Pro	Leu	Asp	275	280	285
Leu	Ser	Gly	Asp	Lys	Ser	Asn	Phe	Val	Leu	Arg	Ser	Thr	Gln	Tyr	Ala	290	295	300
Gln	Thr	Asp	Leu	Glu	Asp	Pro	His	Leu	Thr	Leu	Ala	Asp	Val	Arg	Glu	305	310	315
Lys	Met	Arg	Met	Glu	Ala	Glu	Glu	Arg	Glu	Ala	Gln	Asn	Arg	Ile	Glu	325	330	335
Asn	Glu	Ala	Leu	Glu	Glu	Val	Thr	Ile	Pro	Ile	Asp	Asn	Glu	Asp	Ala	340	345	350
Thr	Glu	Ser	Leu	Asn	Lys	Gln	Glu	Pro	Ser	Ser	Leu	Glu	Leu	Pro	Ile	355	360	365
His	Asn	Val	Ala	Asp	Leu	Ser	Lys	Glu	Pro	Glu	Leu	Met	Glu	Ala	Ala	370	375	380
Ser	Glu	Ala	Thr	Ala	Leu	Glu	Met	Thr	Val	Ala	Ser	Leu	Glu	Ser	Met	385	390	395
Glu	Asn	Ala	Leu	Leu	Asn	Gln	Gln	Ala	Asn	Lys	Glu	Pro	Thr	Pro	Pro	405	410	415

Cura 468 SEQ list 0405.txt

Ser	Thr	Val	Ile	Lys	Pro	Leu	Ala	Glu	Ile	Leu	Lys	Lys	Pro	Gln	Pro		
			420					425					430				
Leu	Asn	Pro	Leu	Ser	Gly	Asn	Asn	Val	Gln	Asn	Ser	Pro	Leu	Lys	Tyr		
		435					440					445					
Ser	Ser	Val	Leu	Asn	Arg	Pro	Ser	Lys	Lys	Met	Ile	Pro	Pro	Pro	Gly		
	450					455					460						
Gly	Val	Ala	Ala	Gln	Lys	Thr	Ile	Ser	Thr	Lys	Pro	Gly	Leu	Val	Lys		
465					470					475					480		
Pro	Asn	Leu	Thr	Thr	Thr	Val	Asn	Gly	Leu	Arg	Ser	Thr	Lys	Thr	Ala		
				485					490					495			
Thr	Ala	Pro	Pro	Ala	Ile	Lys	Thr	Thr	Gly	Arg	Ser	Gly	Leu	Gln	Arg		
			500					505					510				
His	Pro	Arg	Pro	Ser	Ser	Lys	Thr	Glu	Cys	Tyr	Gly	Pro	Pro	Asn	Asn		
		515					520					525					
Val	Ala	Ser	Arg	Leu	Ser	Ala	Arg	Ser	Arg	Thr	Ile	Asn	Thr	Leu	Lys		
	530					535					540						
Ala	Glu	Asn	Gln	His	Ser	Glu	Pro	Lys	Gln	Ile	Gln	Pro	Pro	Thr	Asp		
545					550					555					560		
Ala	Asp	Asp	Gly	Trp	Leu	Thr	Val	Lys	Asn	Arg	Arg	Arg	Thr	Ser	Met		
				565					570					575			
His	Trp	Ala	Asn	Arg	Phe	Asn	Gln	Pro	Thr	Gly	Tyr	Ala	Ser	Leu	Pro		
			580					585					590				
Thr	Leu	Ala	Leu	Leu	Asn	Glu	Gln	Gln	Lys	Glu	Gln	Glu	His	Lys	Glu		
		595					600					605					
Lys	Gln	Lys	Gly	Glu	Asp	Asp	Gly	Lys	Val	Ile	Val	Lys	Thr	Ile	Ser		
	610					615					620						
Ala	Lys	Thr	Lys	Ala	Pro	Ile	Glu	Val	Ala	Lys	Ala	Lys	Ala	Lys	Thr		
625					630					635					640		
Ser	Ile	Val	Ile	Thr	Arg	Pro	Glu	Ile	Lys	Asn	Ala	Lys	Ala	Lys	Val		
				645					650					655			
Asn	Ser	Phe	Pro	Val	Gln	Lys	Ser	Asn	Thr	Asn	Gln	Val	Lys	Lys	Pro		
			660					665					670				

Cura 468 SEQ list 0405.txt

Glu	Lys	Gln	Glu	Lys	Ser	Asp	Thr	Thr	Ala	Pro	Ala	Ala	Ile	Ala	Ser	
		675					680					685				
Ser	Arg	Leu	Lys	Met	Thr	Ser	Leu	His	Lys	Glu	Tyr	Met	Arg	Ser	Glu	
	690					695					700					
Lys	Asn	Ala	Leu	Arg	Lys	Leu	Gln	Gln	Lys	Glu	Gln	Gly	Asn	Gln	Gln	
705					710					715					720	
His	Asn	Ser	Ser	Ser	Ser	Ser	Ala	Glu	Thr	Val	Val	Glu	Ser	Cys	Asn	
				725					730					735		
Glu	Asp	His	Ser	Lys	Ile	Asp	Ile	Lys	Ile	Gln	Thr	Asn	Cys	Glu	Phe	
			740					745					750			
Ser	Lys	Thr	Ile	Gly	Glu	Leu	Tyr	Glu	Ser	Ile	Ala	His	Cys	Lys	Leu	
		755					760						765			
Pro	Ser	Gly	Ser	Leu	Lys	Thr	Asn	Ala	Ser	Thr	Leu	Ser	Ala	Cys	Asp	
		770				775						780				
Glu	Asn	Glu	Glu	Gln	Asn	Thr	Asp	Asp	Asn	Glu	Glu	Glu	Arg	Asn	Glu	
785					790					795					800	
Arg	Ile	Leu	Gly	Glu	Val	Gln	Glu	Ser	Leu	Glu	Arg	Gln	Ile	Arg	Glu	
				805					810					815		
Leu	Glu	Gln	Thr	Glu	Ile	Asp	Val	Asp	Thr	Glu	Thr	Asp	Glu	Thr	Asp	
			820					825					830			
Cys	Glu	Val	Gln	Leu	Glu	Glu	Gln	Asp	Asp	Gly	Val	Asp	Gly	Leu	Glu	
		835					840					845				
Met	Gly	Ser	Gly	Asp	Asp	Ser	Ala	Val	Phe	Val	Thr	Met	Ser	Asp	Asp	
	850					855					860					
Glu	Asn	Ala	Ser	Leu	Glu	Leu	Arg	Tyr	Gln	Ala	Leu	Leu	Ser	Asp	Met	
865					870					875					880	
Ser	Trp	Asn	Glu	Arg	Ala	Glu	Ala	Leu	Ala	Thr	Leu	Gln	Ala	Tyr	Val	
				885					890					895		
Ala	Arg	His	Pro	Gly	Arg	Ala	Gln	Glu	Leu	His	Gln	Lys	Leu	Ser	Ser	
			900					905					910			
Pro	Ser	Arg	Arg	Arg	Ser	Leu	Gln	Glu	Thr	Leu	Lys	Lys	Tyr	Gln	Ala	
		915					920					925				

Cura 468 SEQ list 0405.txt

Lys	Gln	Ala	Arg	Ala	Gln	Gln	Lys	Arg	Asn	Leu	Leu	Gln	Gln	Glu	Lys	930	935	940	
Ala	Ala	Lys	Leu	Gln	Gln	Leu	Phe	Ser	Arg	Val	Glu	Asp	Val	Lys	Ala	945	950	955	960
Ala	Lys	Asn	Gln	Ile	Ile	Glu	Asp	Lys	Arg	Gln	Lys	Met	Gln	Gly	Arg	965	970	975	
Leu	Gln	Arg	Ala	Ala	Glu	Asn	Arg	Glu	Gln	Tyr	Leu	Lys	Gln	Ile	Ile	980	985	990	
Glu	Lys	Ala	His	Asp	Glu	Glu	Lys	Lys	Leu	Lys	Glu	Ile	Asn	Phe	Ile	995	1000	1005	
Lys	Asn	Ile	Glu	Ala	Gln	Asn	Lys	Arg	Leu	Asp	Leu	Leu	Glu	Ser	Ser	1010	1015	1020	
Lys	Glu	Thr	Glu	Gly	Arg	Leu	Gln	Asp	Leu	Glu	Gln	Glu	Arg	Gln	Lys	1025	1030	1035	1040
Arg	Val	Glu	Glu	Lys	Leu	Ala	Lys	Glu	Ala	Ala	Val	Glu	Arg	Arg	Arg	1045	1050	1055	
Gln	Ala	Leu	Glu	Lys	Glu	Arg	Leu	Leu	Lys	Leu	Glu	Lys	Met	Asn	Glu	1060	1065	1070	
Thr	Arg	Leu	Glu	Lys	Glu	Gln	Arg	Ile	Gly	Lys	Met	Gln	Glu	Gln	Lys	1075	1080	1085	
Glu	Lys	Gln	Arg	Gln	Ala	Leu	Ala	Arg	Glu	Lys	Ala	Arg	Asp	Arg	Glu	1090	1095	1100	
Glu	Arg	Leu	Leu	Ala	Leu	Gln	Val	Gln	Gln	Gln	Gln	Thr	Thr	Glu	Glu	1105	1110	1115	1120
Leu	Gln	Arg	Lys	Ile	Leu	Gln	Lys	Gln	Met	Glu	Ser	Ala	Arg	Arg	His	1125	1130	1135	
Glu	Glu	Asn	Ile	Glu	His	Ile	Arg	Gln	Arg	Ala	Leu	Glu	Leu	Thr	Ile	1140	1145	1150	
Pro	Thr	Arg	Gln	Ala	Asp	Glu	Gly	Arg	Gly	Asp	Gln	Asp	Val	Ser	Glu	1155	1160	1165	
Asp	Ile	Leu	Asn	Gly	Asn	Ala	Thr	Ser	Thr	Thr	Asn	Glu	Asp	Cys	Asp	1170	1175	1180	

Cura 468 SEQ list 0405.txt

Leu	Ser	Ser	Ser	Leu	Ser	Glu	Val	Gly	Gly	Asn	Asn	Ala	His	Thr	Arg	1185	1190	1195	1200
Ser	Tyr	Lys	Lys	Lys	Met	Lys	Lys	Leu	Lys	Gln	Arg	Met	Asn	Gln	Cys	1205	1210	1215	
Ala	Ala	Glu	Tyr	Leu	Glu	Ser	Leu	Glu	Ala	Leu	Pro	Ala	His	Ala	Arg	1220	1225	1230	
Arg	Asp	Ser	Thr	Val	Pro	Lys	Leu	Leu	Asn	Leu	Val	Val	Lys	Gly	Gly	1235	1240	1245	
Gly	Ala	Gln	Gly	Leu	Asp	Arg	Asn	Leu	Gly	Asn	Leu	Leu	Arg	Val	Ile	1250	1255	1260	
Pro	Lys	Ala	Gln	Thr	Leu	Asp	Phe	Leu	Ala	Phe	Leu	Cys	Met	Asp	Gly	1265	1270	1275	1280
Leu	Gly	Ile	Leu	Ala	Asn	His	Val	Ile	Ser	Lys	Gly	Met	Asp	Glu	Asn	1285	1290	1295	
Ser	Glu	Ile	Ser	Arg	Lys	Ser	Val	Tyr	Leu	Ala	Ala	Gln	Leu	Tyr	Arg	1300	1305	1310	
Asn	Ala	Cys	Ser	Val	Cys	Pro	Gln	Ile	Ala	Arg	His	Ala	Leu	Leu	Gly	1315	1320	1325	
Asn	Ser	Ile	Thr	Val	Leu	Phe	Asp	Ala	Ile	Asn	Lys	Ser	Phe	Gln	Val	1330	1335	1340	
Ile	Leu	Lys	Ser	Asn	Arg	Cys	Thr	Lys	Glu	Thr	Phe	Ser	Asn	Phe	Trp	1345	1350	1355	1360
Pro	Pro	Lys	Met	Leu	His	Asn	Lys	Ser	Val	Ala	Arg	Gln	Ser	Ser	Arg	1365	1370	1375	
Leu	Glu	Ala	Leu	Ser	Leu	Pro	Glu	Glu	Lys	Ser	Pro	Gln	His	Pro	Val	1380	1385	1390	
Glu	Leu	Ser	Thr	Glu	Leu	Met	Leu	Ala	Cys	Thr	Glu	Ala	Leu	Ser	Ser	1395	1400	1405	
Ser	Tyr	Val	Lys	Lys	Asn	Thr	His	Pro	Lys	Val	Pro	Glu	Arg	Leu	Pro	1410	1415	1420	
Asp	Met	Ile	Asn	Asp	Cys	Arg	Phe	His	Trp	Gln	Asp	Val	Asn	Lys	Glu	1425	1430	1435	1440

Cura 468 SEQ list 0405.txt

Asp Met Leu Ala Asp	Glu Phe Arg Lys Tyr	Lys Cys Tyr Glu Lys Asn
1445	1450	1455
Pro Val Ile Ala Leu	Pro His Pro Ser Leu	Ser Ala Ser Leu Cys Arg
1460	1465	1470
Ser Leu Ser Ala Thr	Pro Leu Lys Ile Asn	Leu His Gln Phe Leu Gly
1475	1480	1485
Ser Gly Ile Leu Ile	Leu Arg Leu Asn His	His Arg His Pro Ala Thr
1490	1495	1500
Gly Ala Ser Phe Ser	Asp Ser Cys Cys Thr	Cys Cys Pro Lys Leu Thr
1505	1510	1520
Thr Glu Ala Ala Val	Ala Ala Val Ala Ala	His Gln His Gln His Gln
1525	1530	1535
Asn Gln Gln Gln Gln	Pro Asp Tyr Ala Val	Ile Thr Gly Leu Ile Glu
1540	1545	1550
Ile Leu Ser Arg Arg	Ile Gln Lys Val Arg	Glu Ser Ile Glu Ser Asn
1555	1560	1565
Lys Ser Val Met Leu	Ser Leu Leu Thr Thr	Leu Gly Phe Leu Ser Arg
1570	1575	1580
Phe Ile Asp Val Cys	Gln Pro Gly Pro Ala	Asp Pro Thr Arg Leu Leu
1585	1590	1600
Ser Ala Ala Lys Ser	Thr Glu Leu Phe Gly	Thr Val Ser Met Leu Tyr
1605	1610	1615
Gly Cys Val Met Pro	Met Gly Glu Cys Ile	Pro Pro Arg Thr Thr Ala
1620	1625	1630
Leu Ala Ala Ser Thr	Phe His Leu Tyr Val	Ser Leu Ala Ser Leu Asp
1635	1640	1645
Val Asn Thr Phe Gln	Glu Thr Leu Thr Val	Glu Gly Pro Leu Ser Leu
1650	1655	1660
Lys Leu Leu Asp Val	Met Thr Val Ile Leu	Asn Cys Ser Leu Val Asn
1665	1670	1680
Asp Gln Trp Thr Thr	Asn Ser Glu Ser Cys	Pro Met Leu Ile Asp Leu
1685	1690	1695



Cura 468 SEQ list 0405.txt

Val Ala Ser Met Ala Phe Phe Cys Val Asn Asn Arg Arg His Gln Asp  
1700 1705 1710

Leu Leu Ile Ser Glu Gln Tyr Ala Val Ile Phe Lys Arg Met Ala Lys  
1715 1720 1725

Leu Pro Thr Gln Phe Asn Pro Val Ile Tyr Pro Phe Leu Val Thr Val  
1730 1735 1740

Ser Phe Asn Asn Pro Pro Ala Arg Glu Phe Leu Ser Lys Asp Phe Asp  
1745 1750 1755 1760

Leu Thr Phe Leu Asp Glu Tyr Ser Lys Ser Glu Met Ala Gln Arg Asn  
1765 1770 1775

Val Val Ile Lys Leu Ile Asn Ser Arg Thr Lys Asp Lys Ile Ser Ala  
1780 1785 1790

Gly Asn Lys Lys Asn Ala  
1795

<210> 49

<211> 274

<212> PRT

<213> Toxocara canis

<400> 49

Met Ala Gly Ala Gln Lys Leu Leu Gly Arg Leu Gly Gln Ile Gly Val  
1 5 10 15

Ala Leu Ala Val Thr Gly Gly Val Val Gln Ser Ala Leu Tyr Asn Val  
20 25 30

Asp Gly Gly Gln Arg Ala Val Ile Phe Asp Arg Phe Thr Gly Val Lys  
35 40 45

Pro Asp Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln  
50 55 60

Arg Pro Ile Ile Phe Asp Ile Arg Ser Thr Pro Arg Ala Ile Ser Thr  
65 70 75 80

Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Ser Ile Thr Leu Arg Ile  
85 90 95

Leu His Arg Pro Glu Pro Ser Lys Leu Pro Asn Ile Tyr Leu Asn Ile  
100 105 110

Cura 468 SEQ list 0405.txt

Gly	Gln	Asp	Tyr	Ala	Glu	Arg	Val	Leu	Pro	Ser	Ile	Thr	Asn	Glu	Val
		115					120					125			
Leu	Lys	Ala	Val	Val	Ala	Gln	Phe	Asp	Ala	His	Glu	Met	Ile	Thr	Gln
	130					135					140				
Arg	Glu	Ser	Val	Ser	His	Arg	Val	Ser	Val	Glu	Leu	Ser	Glu	Arg	Ala
145					150					155					160
Arg	Gln	Phe	Gly	Ile	Leu	Leu	Asp	Asp	Ile	Ala	Ile	Thr	His	Leu	Ser
				165					170					175	
Phe	Gly	Arg	Glu	Phe	Thr	Glu	Ala	Val	Glu	Met	Lys	Gln	Val	Ala	Gln
			180					185					190		
Gln	Glu	Ala	Glu	Lys	Ala	Arg	Tyr	Leu	Val	Glu	Thr	Ala	Glu	Gln	Met
		195					200					205			
Lys	Ile	Ala	Ala	Ile	Thr	Thr	Ala	Glu	Gly	Asp	Ala	Gln	Ala	Ala	Lys
	210					215					220				
Leu	Leu	Ala	Gln	Ala	Phe	Lys	Asp	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu
225					230					235					240
Arg	Lys	Ile	Glu	Ala	Ala	Glu	Glu	Ile	Ala	Glu	Arg	Met	Ser	Lys	Thr
				245					250					255	
Arg	Asn	Val	Ile	Tyr	Leu	Pro	Gly	Asn	Gln	Asn	Thr	Leu	Phe	Asn	Leu
			260					265					270		

Pro Ala

<210> 50

<211> 402

<212> PRT

<213> Caenorhabditis elegans

<400> 50

Met	Glu	Lys	Tyr	Lys	Asn	Glu	Leu	Glu	Ile	Phe	Lys	Arg	Met	Tyr	Phe
1				5					10					15	

Lys	Asn	Tyr	Pro	Thr	Ser	Ser	Lys	Asp	Glu	Glu	Ala	Ala	Ala	Val	Ile
			20					25					30		

Gln	Lys	Gly	Gly	Glu	Phe	Ile	Gln	Glu	Ile	Leu	Pro	Thr	Ile	Ile	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## Cura 468 SEQ list 0405.txt

35					40					45					
Thr	Ser	Arg	Ala	Tyr	Asp	Thr	Asn	Gln	Lys	Ala	Leu	Leu	Leu	Ala	Glu
	50					55					60				
Gly	Gly	Lys	Met	Tyr	Asn	Val	Leu	Glu	Asp	Tyr	Asn	Glu	Thr	Ala	Glu
65					70					75					80
Lys	Met	Leu	Ser	Lys	Ser	Val	Arg	Met	Asn	Pro	Lys	Asn	Ala	Asp	Ala
				85					90					95	
Trp	His	Glu	Leu	Gly	Leu	Cys	Val	Met	Lys	Arg	Arg	Asp	Leu	Glu	Phe
			100					105					110		
Ala	Gln	Ser	Cys	Phe	Lys	Ile	Ala	Leu	Gly	Ile	Ser	Lys	Thr	Ala	Pro
		115					120					125			
Ile	Leu	Thr	Ser	Leu	Ala	Val	Ala	Met	Arg	Leu	Val	Ala	Leu	Glu	His
	130					135					140				
Pro	Glu	Pro	Ala	Gln	Ala	Glu	Ile	Arg	Thr	Lys	Ala	Met	Glu	Leu	Ile
145						150					155				160
Ile	Glu	Ala	Arg	Arg	Leu	Asp	Ser	Ala	Tyr	Gly	Pro	Ala	Asn	Ile	Ala
				165					170					175	
Phe	Ala	Thr	Gly	Leu	Phe	Tyr	Cys	Phe	Phe	Ser	Thr	Ala	Lys	Val	Glu
			180					185					190		
Leu	Lys	Phe	Leu	Asp	Lys	Val	Ile	Glu	Asn	Tyr	Lys	Lys	Ala	Leu	Glu
		195					200					205			
Cys	Glu	Leu	Ser	Arg	Thr	Asp	Pro	Gln	Val	Tyr	Ile	Asn	Met	Ala	Thr
	210					215					220				
Cys	Leu	Lys	Phe	Met	Glu	Lys	Tyr	Asp	Glu	Ala	Leu	Ala	Val	Leu	Gln
225						230					235				240
Lys	Ala	Val	Glu	Tyr	Asp	Pro	Arg	Asn	Glu	Leu	Glu	Thr	Arg	Glu	Lys
				245					250					255	
Leu	Ala	Ser	Phe	Val	Ser	Tyr	Leu	Ser	Lys	Phe	Thr	Asp	Ala	Ile	Gln
			260					265					270		
Lys	Lys	Gly	Lys	Met	Lys	Ala	Lys	Arg	Met	Gln	Glu	Met	Ile	Asn	Glu
		275					280					285			
Leu	Lys	Lys	Ser	Ser	Asp	Gly	Phe	Arg	Ala	Lys	Ile	Ile	Gly	Asn	Ile

Cura 468 SEQ list 0405.txt

290

295

300

Gly His Asp Glu Thr Ile Pro Val Ala Leu Val Gly Val Asp Ala Ala  
305 310 315 320

Gly Glu Val Tyr Gly Ile Thr Ile Tyr Asn Cys Leu Ser Asn Phe Gly  
325 330 335

Phe Val Ile Gly Asp Thr Val Thr Ile Ala Lys Pro Asp Phe Arg Glu  
340 345 350

Ile Lys Asn Leu Thr Ile Pro Ser Asp Pro Glu Ile His Val Asp Ser  
355 360 365

Val Lys Trp Ile Arg Val Ala Thr Pro Thr Gln Met Lys Lys Asn Gly  
370 375 380

Val Pro Leu Pro Glu Ser Val Leu Ala Arg Ala Val Ala Ser Thr Gln  
385 390 395 400

Thr Lys

<210> 51

<211> 711

<212> PRT

<213> Homo sapiens

<400> 51

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val  
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu  
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly  
85 90 95

Cura 468 SEQ list 0405.txt

Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met	100	105	110
Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly	115	120	125
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr	130	135	140
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	145	150	155
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	165	170	175
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	180	185	190
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	195	200	205
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	210	215	220
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	225	230	235
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	245	250	255
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	260	265	270
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	275	280	285
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	290	295	300
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu	305	310	315
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	325	330	335
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	340	345	350

Cura 468 SEQ list 0405.txt

Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	
		355					360					365				
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys	
	370					375					380					
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His	
385					390					395					400	
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu	
				405					410					415		
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	
			420					425					430			
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys	
		435					440					445				
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln	
	450					455					460					
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser	
465					470					475					480	
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val	
				485					490					495		
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val	
			500					505					510			
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His	
		515					520					525				
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn	
	530					535					540					
Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	Met	
545					550					555					560	
Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	Arg	
				565					570					575		
Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	Glu	
			580					585					590			
Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	Ile	Ala	Gly	Trp	Gly	
		595					600					605				

Cura 468 SEQ list 0405.txt

Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu  
610 615 620

Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val  
625 630 635 640

Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala  
645 650 655

Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys  
660 665 670

Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser  
675 680 685

Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile  
690 695 700

His Lys Val Met Arg Leu Gly  
705 710

<210> 52  
<211> 711  
<212> PRT  
<213> Homo sapiens

<400> 52  
Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val  
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu  
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly  
85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met  
100 105 110

•

Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Val	Gly	Gly	
		115					120					125			
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr
	130					135					140				
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro
145					150					155					160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val
				165					170					175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val
			180					185					190		
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser
		195					200					205			
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro
	210					215					220				
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys
225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
				245					250					255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala
			260					265					270		
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly
		275					280					285			
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys
	290					295					300				
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu
305					310					315					320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp
				325					330					335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala
			340					345					350		
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln
		355					360					365			



## Cura 468 SEQ list 0405.txt

Asp 370	Cys	Tyr	His	Gly	Ala	Gly 375	Glu	Gln	Tyr	Arg	Gly 380	Thr	Val	Ser	Lys
Thr 385	Arg	Lys	Gly	Val	Gln 390	Cys	Gln	Arg	Trp	Ser 395	Ala	Glu	Thr	Pro	His 400
Lys	Pro	Gln	Phe	Thr 405	Phe	Thr	Ser	Glu	Pro 410	His	Ala	Gln	Leu	Glu 415	Glu
Asn	Phe	Cys	Arg 420	Asn	Pro	Asp	Gly	Asp 425	Ser	His	Gly	Pro	Trp 430	Cys	Tyr
Thr	Met	Asp 435	Pro	Arg	Thr	Pro	Phe 440	Asp	Tyr	Cys	Ala	Leu 445	Arg	Arg	Cys
Ala	Asp 450	Asp	Gln	Pro	Pro	Ser 455	Ile	Leu	Asp	Pro	Pro 460	Asp	Gln	Val	Gln
Phe 465	Glu	Lys	Cys	Gly	Lys 470	Arg	Val	Asp	Arg	Leu 475	Asp	Gln	Arg	Arg	Ser 480
Lys	Leu	Arg	Val	Val 485	Gly	Gly	His	Pro	Gly 490	Asn	Ser	Pro	Trp	Thr 495	Val
Ser	Leu	Arg	Asn 500	Arg	Gln	Gly	Gln	His 505	Phe	Cys	Gly	Gly	Ser 510	Leu	Val
Lys	Glu	Gln 515	Trp	Ile	Leu	Thr	Ala 520	Arg	Gln	Cys	Phe	Ser 525	Ser	Cys	His
Met	Pro 530	Leu	Thr	Gly	Tyr	Glu 535	Val	Trp	Leu	Gly	Thr 540	Leu	Phe	Gln	Asn
Pro 545	Gln	His	Gly	Glu	Pro 550	Ser	Leu	Gln	Arg	Val 555	Pro	Val	Ala	Lys	Met 560
Val	Cys	Gly	Pro	Ser 565	Gly	Ser	Gln	Leu	Val 570	Leu	Leu	Lys	Leu	Glu 575	Arg
Ser	Val	Thr	Leu 580	Asn	Gln	Arg	Val	Ala 585	Leu	Ile	Cys	Leu	Pro 590	Pro	Glu
Trp	Tyr	Val 595	Val	Pro	Pro	Gly	Thr 600	Lys	Cys	Glu	Ile	Ala 605	Gly	Trp	Gly
Glu	Thr 610	Lys	Gly	Thr	Gly	Asn 615	Asp	Thr	Val	Leu	Asn 620	Val	Ala	Phe	Leu

Cura 468 SEQ list 0405.txt

Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val  
625 630 635 640

Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala  
645 650 655

Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys  
660 665 670

Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser  
675 680 685

Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile  
690 695 700

His Lys Val Met Arg Leu Gly  
705 710

<210> 53

<211> 711

<212> PRT

<213> Homo sapiens

<400> 53

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Tyr Leu Gly Val  
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu  
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly  
85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met  
100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly

115 120 125

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Cura 468 SEQ list 0405.txt

370																
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His	
385					390					395					400	
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu	
				405					410					415		
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	
			420					425					430			
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys	
		435					440					445				
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln	
	450					455					460					
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser	
465					470					475					480	
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val	
				485					490					495		
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val	
			500					505					510			
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His	
		515					520					525				
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn	
	530					535					540					
Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	Met	
545					550					555					560	
Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	Arg	
				565					570					575		
Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	Glu	
			580					585					590			
Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	Ile	Ala	Gly	Trp	Gly	
		595					600					605				
Glu	Thr	Lys	Gly	Thr	Gly	Asn	Asp	Thr	Val	Leu	Asn	Val	Ala	Leu	Leu	
	610					615					620					
Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Ile	Lys	His	Arg	Gly	Arg	Val	

Cura 468 SEQ list 0405.txt

625 630 635 640

Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala  
645 650 655

Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys  
660 665 670

Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser  
675 680 685

Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile  
690 695 700

His Lys Val Met Arg Leu Gly  
705 710

<210> 54

<211> 529

<212> PRT

<213> Homo sapiens

<400> 54

Met Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln  
1 5 10 15

Leu Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg His Ser  
20 25 30

Gly Arg Cys Asp Leu Phe Gln Glu Lys Asp Tyr Ile Arg Thr Cys Ile  
35 40 45

Met Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly  
50 55 60

Gly Leu Ser Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Gln  
65 70 75 80

Tyr Met Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn  
85 90 95

Pro Asp Gly Asp Pro Gly Gly Pro Trp Cys His Thr Thr Asp Pro Ala  
100 105 110

Val Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Val Ala Ala Cys  
115 120 125

Cura 468 SEQ list 0405.txt

Val	Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	130	135	140
Ser	Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	145	150	155
Pro	Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	165	170	175
Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	180	185	190
Pro	Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	195	200	205
Ala	Gln	Pro	Arg	Gln	Glu	Ala	Thr	Ser	Val	Ser	Cys	Phe	Arg	Gly	Lys	210	215	220
Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	225	230	235
Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	245	250	255
Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	260	265	270
Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	275	280	285
Val	Gly	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	290	295	300
Gln	Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	305	310	315
Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Gly	Ser	Ala	Glu	Thr	Pro	325	330	335
His	Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	340	345	350
Glu	Asn	Phe	Cys	Gln	Thr	Gln	Met	Gly	Ile	Ala	Met	Gly	Pro	Gly	Ala	355	360	365
Thr	Arg	Trp	Thr	Gln	Gly	Pro	His	Ser	Thr	Thr	Val	Pro	Cys	Asp	Ala	370	375	380

Cura 468 SEQ list 0405.txt

Ala	Leu	Met	Thr	Ser	Arg	His	Gln	Ser	Trp	Thr	Pro	Gln	Thr	Arg	Cys
385					390					395					400
Ser	Leu	Arg	Ser	Val	Ala	Arg	Gly	Trp	Ile	Gly	Trp	Ile	Ser	Val	Val
				405					410					415	
Pro	Ser	Cys	Ala	Trp	Leu	Gly	Ala	Ile	Arg	Ala	Thr	His	Pro	Gly	Gln
			420					425					430		
Ser	Ala	Cys	Gly	Ile	Gly	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu
		435					440					445			
Val	Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys
	450					455					460				
His	Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln
465					470					475					480
Asn	Pro	Gln	His	Gly	Glu	Pro	Gly	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys
				485					490					495	
Met	Leu	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu
			500					505					510		
Arg	Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro
		515					520					525			

Glu

<210> 55  
 <211> 716  
 <212> PRT  
 <213> Mus musculus

<400> 55
Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Val Gln Cys Ser Arg Ala
1 5 10 15
Leu Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Leu Phe Arg Gly Thr
20 25 30
Glu Leu Arg Asn Leu Leu His Thr Ala Val Pro Gly Pro Trp Gln Glu
35 40 45
Asp Val Ala Asp Ala Glu Glu Cys Ala Arg Arg Cys Gly Pro Leu Leu
50 55 60

Cura 468 SEQ list 0405.txt

Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Met	Ser	Ser	His	Gly	Cys	Gln	Leu
65					70					75					80
Leu	Pro	Trp	Thr	Gln	His	Ser	Leu	His	Thr	Gln	Leu	Tyr	His	Ser	Ser
				85					90					95	
Leu	Cys	His	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met
			100					105					110		
Asp	Asn	Gly	Val	Ser	Tyr	Arg	Gly	Thr	Val	Ala	Arg	Thr	Ala	Gly	Gly
		115					120					125			
Leu	Pro	Cys	Gln	Ala	Trp	Ser	Arg	Arg	Phe	Pro	Asn	Asp	His	Lys	Tyr
	130					135					140				
Thr	Pro	Thr	Pro	Lys	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro
145					150					155					160
Asp	Gly	Asp	Pro	Arg	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asn	Arg	Ser	Val
				165					170					175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Thr	Cys	Arg	Glu	Ala	Val	Cys	Val
			180					185					190		
Leu	Cys	Asn	Gly	Glu	Asp	Tyr	Arg	Gly	Glu	Val	Asp	Val	Thr	Glu	Ser
		195					200					205			
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Ser	His	Pro
	210					215					220				
Phe	Gln	Pro	Glu	Lys	Phe	Leu	Asp	Lys	Asp	Leu	Lys	Asp	Asn	Tyr	Cys
225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
				245					250					255	
Asn	Val	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Ser	Cys	Gly	Pro	Asn	Leu
			260					265					270		
Pro	Pro	Thr	Val	Lys	Gly	Ser	Lys	Ser	Gln	Arg	Arg	Asn	Lys	Gly	Lys
		275					280					285			
Ala	Leu	Asn	Cys	Phe	Arg	Gly	Lys	Gly	Glu	Asp	Tyr	Arg	Gly	Thr	Thr
	290					295					300				
Asn	Thr	Thr	Ser	Ala	Gly	Val	Pro	Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ser
305					310					315					320



Cura 468 SEQ list 0405.txt

Pro	His	Gln	His	Arg	Phe	Val	Pro	Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	325	330	335
Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	340	345	350
Phe	Thr	Ser	Arg	Pro	Gly	Leu	Arg	Met	Ala	Phe	Cys	His	Gln	Ile	Pro	355	360	365
Arg	Cys	Thr	Glu	Glu	Leu	Val	Pro	Glu	Gly	Cys	Tyr	His	Gly	Ser	Gly	370	375	380
Glu	Gln	Tyr	Arg	Gly	Ser	Val	Ser	Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	385	390	400
Gln	His	Trp	Ser	Ser	Glu	Thr	Pro	His	Lys	Pro	Gln	Phe	Thr	Pro	Thr	405	410	415
Ser	Ala	Pro	Gln	Ala	Gly	Leu	Glu	Ala	Asn	Phe	Cys	Arg	Asn	Pro	Asp	420	425	430
Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	Thr	Leu	Asp	Pro	Asp	Ile	Leu	435	440	445
Phe	Asp	Tyr	Cys	Ala	Leu	Gln	Arg	Cys	Asp	Asp	Asp	Gln	Pro	Pro	Ser	450	455	460
Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Val	Phe	Glu	Lys	Cys	Gly	Lys	Arg	465	470	480
Val	Asp	Lys	Ser	Asn	Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	485	490	495
Ser	Pro	Trp	Thr	Val	Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	500	505	510
Gly	Gly	Ser	Leu	Val	Lys	Glu	Gln	Trp	Val	Leu	Thr	Ala	Arg	Gln	Cys	515	520	525
Ile	Trp	Ser	Cys	His	Glu	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	530	535	540
Thr	Ile	Asn	Gln	Asn	Pro	Gln	Pro	Gly	Glu	Ala	Asn	Leu	Gln	Arg	Val	545	550	555
Pro	Val	Ala	Lys	Ala	Val	Cys	Gly	Pro	Ala	Gly	Ser	Gln	Leu	Val	Leu	565	570	575

Cura 468 SEQ list 0405.txt

Leu	Lys	Leu	Glu	Arg	Pro	Val	Ile	Leu	Asn	His	His	Val	Ala	Leu	Ile
			580					585					590		
Cys	Leu	Pro	Pro	Glu	Gln	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu
		595					600					605			
Ile	Ala	Gly	Trp	Gly	Glu	Ser	Ile	Gly	Thr	Ser	Asn	Asn	Thr	Val	Leu
	610					615					620				
His	Val	Ala	Ser	Met	Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Thr	Lys
625					630					635					640
Tyr	Arg	Gly	His	Ile	Gln	Glu	Ser	Glu	Ile	Cys	Thr	Gln	Gly	Leu	Val
				645					650					655	
Val	Pro	Val	Gly	Ala	Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys
			660					665					670		
Tyr	Thr	His	Asp	Cys	Trp	Val	Leu	Gln	Gly	Leu	Ile	Ile	Pro	Asn	Arg
		675					680					685			
Val	Cys	Ala	Arg	Pro	Arg	Trp	Pro	Ala	Ile	Phe	Thr	Arg	Val	Ser	Val
	690					695					700				
Phe	Val	Asp	Trp	Ile	Asn	Lys	Val	Met	Gln	Leu	Glu				
705					710					715					

<210> 56  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 56

Met	Ala	Thr	Val	Gln	Gln	Leu	Glu	Gly	Arg	Trp	Arg	Leu	Val	Asp	Ser
1				5					10					15	
Lys	Gly	Phe	Asp	Glu	Tyr	Met	Lys	Glu	Leu	Gly	Val	Gly	Ile	Ala	Leu
			20					25					30		
Arg	Lys	Met	Gly	Ala	Met	Ala	Lys	Pro	Asp	Cys	Ile	Val	Thr	Cys	Asp
		35					40					45			
Gly	Lys	Asn	Leu	Thr	Ile	Lys	Thr	Glu	Ser	Thr	Leu	Lys	Thr	Thr	Gln
	50					55					60				
Phe	Ser	Cys	Pro	Leu	Gly	Glu	Lys	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly

Cura 468 SEQ list 0405.txt

65		70		75		80									
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
			85						90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Ser	Thr	Ile	Thr	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Glu	Cys	Val	Met	Asn	His	Val	Ala	Cys	Thr
		115					120					125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
	130					135									

<210> 57  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 57

Met	Ala	Thr	Val	Gln	Gln	Leu	Glu	Gly	Arg	Trp	Arg	Leu	Val	Asp	Ser
1				5					10					15	
Lys	Gly	Phe	Asp	Glu	Tyr	Met	Lys	Glu	Leu	Gly	Val	Gly	Ile	Ala	Leu
			20					25					30		
Arg	Lys	Met	Gly	Ala	Met	Ala	Lys	Pro	Asp	Cys	Ile	Ile	Thr	Cys	Asp
		35					40					45			
Gly	Lys	Asn	Leu	Thr	Ile	Lys	Thr	Glu	Ser	Thr	Leu	Lys	Thr	Thr	Gln
		50				55					60				
Phe	Ser	Cys	Thr	Leu	Gly	Glu	Lys	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly
65					70					75					80
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
			85						90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Ser	Thr	Ile	Thr	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Glu	Cys	Val	Met	Asn	Asn	Val	Thr	Cys	Thr
		115					120					125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
	130					135									

Cura 468 SEQ list 0405.txt

<210> 58  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser  
 1 5 10 15  
 Arg Gly Phe Asp Glu Tyr Val Lys Glu Leu Gly Val Gly Ile Ala Leu  
 20 25 30  
 Arg Lys Met Asp Thr Ile Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp  
 35 40 45  
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln  
 50 55 60  
 Phe Ser Cys Thr Leu Gly Glu Asn Phe Glu Glu Thr Thr Ala Asp Gly  
 65 70 75 80  
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln  
 85 90 95  
 His Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Arg Arg Lys Leu Lys  
 100 105 110  
 Asp Gly Lys Leu Val Val Asp Cys Val Met Asn Ser Val Thr Cys Thr  
 115 120 125  
 Arg Ile Tyr Glu Lys Val Glu  
 130 135

<210> 59  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 59  
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Leu Asp Ser  
 1 5 10 15  
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu  
 20 25 30  
 Gln Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp

Cura 468 SEQ list 0405.txt

35		40		45											
Gly	Arg	Asn	Leu	Thr	Thr	Lys	Thr	Glu	Ser	Thr	Leu	Lys	Thr	Thr	Gln
	50					55					60				
Phe	Ser	Cys	Thr	Leu	Gly	Asp	Glu	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly
65					70					75					80
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
				85					90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Ser	Thr	Ile	Thr	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Glu	Cys	Val	Met	Asn	Asn	Val	Thr	Cys	Thr
	115						120					125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
130						135									

<210> 60  
 <211> 135  
 <212> PRT  
 <213> Bos taurus

<400> 60															
Met	Ala	Thr	Val	Gln	Gln	Leu	Val	Gly	Arg	Trp	Arg	Leu	Val	Glu	Ser
1				5					10					15	
Lys	Gly	Phe	Asp	Glu	Tyr	Met	Lys	Glu	Val	Gly	Val	Gly	Met	Ala	Leu
			20					25					30		
Arg	Lys	Val	Gly	Ala	Met	Ala	Lys	Pro	Asp	Cys	Ile	Ile	Thr	Ser	Asp
		35					40					45			
Gly	Lys	Asn	Leu	Ser	Ile	Lys	Thr	Glu	Ser	Thr	Leu	Lys	Thr	Thr	Gln
	50					55					60				
Phe	Ser	Cys	Lys	Leu	Gly	Glu	Lys	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly
65					70					75					80
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
				85					90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Ser	Thr	Ile	Thr	Arg	Lys	Leu	Glu
		100						105					110		

Cura 468 SEQ list 0405.txt

Asp Gly Lys Leu Val Val Val Cys Val Met Asn Asn Val Thr Cys Thr  
 115 120 125

Arg Val Tyr Glu Lys Val Glu  
 130 135

<210> 61  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 61

Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr  
 1 5 10 15

Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg  
 20 25 30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln  
 35 40 45

Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys  
 50 55 60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
 65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
 85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn  
 100 105 110

Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp  
 115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly  
 130 135 140

Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg  
 145 150 155 160

Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr  
 165 170 175

Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr  
 180 185 190

Cura 468 SEQ list 0405.txt

Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Phe	Tyr	Leu	
		195					200					205				
Val	Gly	Lys	Arg	Cys	Met	Glu	Ile	Phe	Gly	Pro	Arg	His	Arg	Arg	Pro	
	210					215					220					
Arg	Cys	Arg	Glu	Cys	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Leu	Ser	
225					230					235					240	
Gln	Gly	Gly	His	Pro	Glu	Asp	Gly	Asn	Ser	Val	Leu	Met	Lys	Ala	Gly	
				245					250						255	
Ser	Ala	Pro	Val	Asp	Ala	Gly	Gly	Tyr	Pro							
			260					265								

<210> 62

<211> 265

<212> PRT

<213> Rattus norvegicus

<400> 62

Met	Asn	Trp	Gly	Phe	Leu	Gln	Gly	Ile	Leu	Ser	Gly	Val	Asn	Lys	Tyr	
1				5					10					15		
Ser	Thr	Ala	Leu	Gly	Arg	Ile	Trp	Leu	Ser	Val	Val	Phe	Ile	Phe	Arg	
			20					25					30			
Val	Leu	Val	Tyr	Val	Val	Ala	Ala	Glu	Glu	Val	Trp	Asp	Asp	Glu	Gln	
		35					40					45				
Lys	Asp	Phe	Ile	Cys	Asn	Thr	Lys	Gln	Pro	Gly	Cys	Pro	Asn	Val	Cys	
	50					55					60					
Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln	
65					70					75					80	
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala	
				85					90					95		
Tyr	Arg	Glu	Glu	Arg	Glu	Arg	Lys	His	Arg	Leu	Lys	His	Gly	Pro	Asp	
			100					105					110			
Ala	Pro	Ala	Leu	Tyr	Ser	Asn	Leu	Ser	Lys	Lys	Arg	Gly	Gly	Leu	Trp	
		115					120					125				
Trp	Thr	Tyr	Leu	Leu	Ser	Leu	Ile	Phe	Lys	Ala	Ala	Val	Asp	Ser	Gly	

Cura 468 SEQ list 0405.txt

130

135

140

Phe	Leu	Tyr	Ile	Phe	His	Cys	Ile	Tyr	Lys	Asp	Tyr	Asp	Met	Pro	Arg
145					150					155					160
Val	Val	Ala	Cys	Ser	Val	Gln	Pro	Cys	Pro	His	Thr	Val	Asp	Cys	Tyr
				165					170					175	
Ile	Ser	Arg	Pro	Thr	Glu	Lys	Lys	Val	Phe	Thr	Tyr	Phe	Met	Val	Val
			180					185					190		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Ala	Tyr	Leu
		195					200					205			
Val	Gly	Lys	Arg	Cys	Met	Glu	Val	Phe	Arg	Pro	Arg	Arg	Gln	Lys	Thr
	210					215					220				
Ser	Arg	Arg	His	Gln	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Ile	Ser
225					230					235					240
Lys	Gly	His	Pro	Gln	Asp	Glu	Ser	Thr	Val	Leu	Thr	Lys	Ala	Gly	Met
				245					250					255	
Ala	Thr	Val	Asp	Ala	Gly	Val	Tyr	Pro							
			260					265							

<210> 63

<211> 266

<212> PRT

<213> Mus musculus

<400> 63

Met	Asn	Trp	Gly	Phe	Leu	Gln	Gly	Ile	Leu	Ser	Gly	Val	Asn	Lys	Tyr
1				5					10					15	
Ser	Thr	Ala	Leu	Gly	Arg	Ile	Trp	Leu	Ser	Val	Val	Phe	Ile	Phe	Arg
			20					25					30		
Val	Leu	Val	Tyr	Val	Val	Ala	Ala	Glu	Glu	Val	Trp	Asp	Asp	Asp	Gln
		35					40					45			
Lys	Asp	Phe	Ile	Cys	Asn	Thr	Lys	Gln	Pro	Gly	Cys	Pro	Asn	Val	Cys
	50					55					60				
Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
65					70					75					80



Cura 468 SEQ list 0405.txt

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asn  
100 105 110

Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly  
130 135 140

Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg  
145 150 155 160

Val Val Ala Cys Ser Val Thr Pro Cys Pro His Thr Val Asp Cys Tyr  
165 170 175

Ile Ala Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val  
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Val Tyr Leu  
195 200 205

Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Arg Lys Ala  
210 215 220

Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser  
225 230 235 240

Lys Gly Gly His Pro Gln Asp Glu Ser Val Ile Leu Thr Lys Ala Gly  
245 250 255

Met Ala Thr Val Asp Ala Gly Val Tyr Pro  
260 265

<210> 64

<211> 273

<212> PRT

<213> Homo sapiens

<400> 64

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg  
20 25 30

Cura 468 SEQ list 0405.txt

Val	Leu	Val	Tyr	Leu	Val	Thr	Ala	Glu	Arg	Val	Trp	Ser	Asp	Asp	His
	35						40					45			
Lys	Asp	Phe	Asp	Cys	Asn	Thr	Arg	Gln	Pro	Gly	Cys	Ser	Asn	Val	Cys
	50					55					60				
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
65					70					75					80
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				85					90					95	
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn
			100					105					110		
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp
		115					120					125			
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala
	130					135					140				
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro
145					150					155					160
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe
				165					170					175	
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala
			180					185					190		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
		195					200					205			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
		210				215					220				
Met	Cys	Thr	Gly	His	His	Pro	His	Gly	Thr	Thr	Ser	Ser	Cys	Lys	Gln
225					230					235					240
Asp	Asp	Leu	Leu	Ser	Gly	Asp	Leu	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His
				245					250					255	
Pro	Pro	Leu	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile
			260					265					270		
Leu															

## Cura 468 SEQ list 0405.txt

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<210> 65
<211> 273
<212> PRT
<213> Homo sapiens
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<220>
<221> VARIANT
<222> (41)
<223> Wherein Xaa is any amino acid.
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<400> 65

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg  
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Xaa Arg Val Trp Ser Asp Asp His  
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys  
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn  
100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala  
130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro  
145 150 155 160

Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe
				165					170					175	

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala  
180 185 190

Cura 468 SEQ list 0405.txt

Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
		195					200					205			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
	210					215					220				
Met	Cys	Thr	Gly	His	His	Pro	His	Gly	Thr	Thr	Ser	Ser	Cys	Lys	Gln
225					230					235					240
Asp	Asp	Leu	Leu	Ser	Gly	Asp	Leu	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His
				245					250					255	
Pro	Pro	Leu	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile
		260						265					270		

Leu

<210> 66  
 <211> 434  
 <212> PRT  
 <213> Homo sapiens

<400> 66

Ala	Lys	Gln	Gln	Leu	Asn	Leu	Arg	Thr	His	Met	Ala	Asp	Glu	Asn	Lys
1				5					10					15	
Asn	Glu	Tyr	Ala	Ala	Gln	Leu	Gln	Asn	Phe	Asn	Gly	Glu	Gln	His	Lys
			20				25						30		
His	Phe	Tyr	Val	Val	Ile	Pro	Gln	Ile	Tyr	Lys	Gln	Leu	Gln	Glu	Met
		35					40					45			
Asp	Glu	Arg	Arg	Thr	Ile	Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe	Ala
	50					55					60				
Asp	Ser	Glu	Arg	Lys	Val	Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu	Gly
65					70					75					80
Met	Ile	Leu	Ala	Ala	Lys	Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln	Met
				85					90					95	
Val	Val	Asp	Ser	Phe	Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe	Pro
			100					105					110		
Phe	Glu	Asp	Tyr	Ser	Gln	His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly	Thr

Cura 468 SEQ list 0405.txt

115																	
Ile	Ser	Ala	Ser	Lys	Gln	Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr	Thr		
130						135					140						
Val	Gly	Lys	Ala	Lys	Gly	Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro	Lys		
145					150					155							160
Pro	Gln	Ser	Pro	Pro	Leu	Thr	Pro	Thr	Ser	Leu	Phe	Thr	Ser	Ser	Thr		
				165					170					175			
Pro	Asn	Gly	Ser	Gln	Phe	Leu	Thr	Phe	Ser	Ile	Glu	Pro	Val	His	Tyr		
			180					185					190				
Cys	Met	Asn	Glu	Ile	Lys	Thr	Gly	Lys	Pro	Arg	Ile	Pro	Ser	Phe	Arg		
		195					200					205					
Ser	Leu	Lys	Arg	Gly	Gly	Pro	Ala	Leu	Glu	Asp	Phe	Ser	His	Leu	Pro		
	210					215					220						
Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Asn		
225					230					235							240
Arg	Glu	Leu	Gln	Lys	Glu	Ser	Asp	Gln	Lys	Asp	Ala	Leu	Asn	Lys	Met		
				245					250					255			
Lys	Asp	Val	Tyr	Glu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Gly	Ser	Leu		
			260					265					270				
Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	Arg	Met		
		275					280					285					
Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	Lys	Thr		
	290					295					300						
Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	Leu	Val		
305					310					315					320		
Thr	Gln	Gly	Arg	Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	Ala	Asn		
				325					330					335			
Gln	Glu	Val	Arg	Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	Glu	Phe		
			340					345					350				
Asp	Asp	Glu	Phe	Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	His	Cys		
		355					360					365					
Lys	Ala	Ile	Tyr	Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	Ala	Met		

Cura 468 SEQ list 0405.txt

370

375

380

Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly  
385 390 395 400

Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr  
405 410 415

Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser Lys Gly Ala Val Thr  
420 425 430

Tyr Ile

<210> 67

<211> 330

<212> PRT

<213> Homo sapiens

<400> 67

Met Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe  
1 5 10 15

Ala Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu  
20 25 30

Gly Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln  
35 40 45

Met Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe  
50 55 60

Pro Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly  
65 70 75 80

Thr Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr  
85 90 95

Thr Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro  
100 105 110

Lys Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro Pro Glu Gln Arg  
115 120 125

Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn Arg Glu Leu Gln  
130 135 140

Cura 468 SEQ list 0405.txt

Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met Lys Asp Val Tyr  
145 150 155 160

Glu Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu Gln Pro Lys Leu  
165 170 175

Ala Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met Glu Ile His Lys  
180 185 190

Asn Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr Gly Gly Arg Gly  
195 200 205

Asp Arg Arg His Ser Ser Asp Ile Asn His Leu Val Thr Gln Gly Arg  
210 215 220

Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp Ala Asn Gln Glu Val Arg  
225 230 235 240

Gly Pro Pro Gln Gln His Gly His His Asn Glu Phe Asp Asp Glu Phe  
245 250 255

Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly His Cys Lys Ala Ile Tyr  
260 265 270

Pro Phe Asp Gly His Asn Glu Gly Thr Leu Ala Met Lys Glu Gly Glu  
275 280 285

Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ala  
290 295 300

Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr Ser Tyr Ile Asp  
305 310 315 320

Val Thr Leu Glu Lys Asn Ser Lys Gly Ser  
325 330

<210> 68

<211> 592

<212> PRT

<213> Homo sapiens

<400> 68

Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys  
1 5 10 15

His Thr Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val  
20 25 30

Cura 468 SEQ list 0405.txt

Lys	Glu	Arg	Thr	Glu	Ile	Glu	Leu	Ser	Tyr	Ala	Lys	Gln	Leu	Arg	Asn	
		35					40					45				
Leu	Ser	Lys	Lys	Tyr	Gln	Pro	Lys	Lys	Asn	Ser	Lys	Glu	Glu	Glu	Glu	
	50					55					60					
Tyr	Lys	Tyr	Thr	Ser	Cys	Lys	Ala	Phe	Ile	Ser	Asn	Leu	Asn	Glu	Met	
65					70					75					80	
Asn	Asp	Tyr	Ala	Gly	Gln	His	Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	
				85					90					95		
Gln	Ile	Ile	Val	Asp	Leu	Ala	Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	
			100					105					110			
Arg	Lys	Ser	Asn	Phe	His	Asp	Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	
		115					120					125				
Thr	Cys	Trp	Lys	Gln	Leu	Glu	Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	
	130					135					140					
Cys	Lys	Glu	Ala	Asp	Arg	Ala	Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	
145					150					155					160	
Asp	Ile	Asn	Val	Thr	Lys	Ala	Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	
				165					170					175		
Gln	Ile	Arg	His	Gln	Met	Ala	Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	
			180					185					190			
Ile	Leu	Gln	Lys	Phe	Asn	His	Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	
		195					200					205				
Ile	Pro	Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	
	210					215					220					
Val	Arg	Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	
225					230					235					240	
Val	Ile	Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	
				245					250					255		
Glu	Ser	Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	
			260					265					270			
Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	
		275					280					285				



Cura 468 SEQ list 0405.txt

Gln	Pro	Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	290	295	300
Gly	Glu	Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	305	310	315
Leu	Trp	Pro	Phe	Ile	Lys	Lys	Asn	Lys	Ser	Pro	Lys	Gln	Gln	Lys	Glu	325	330	335
Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	340	345	350
His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	355	360	365
Thr	Pro	Glu	Asp	Phe	Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	370	375	380
Leu	Gln	Gln	Lys	Val	Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	385	390	395
Asp	Gln	Arg	Asp	Ala	Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	405	410	415
Pro	Gln	Met	Gly	Asp	Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	420	425	430
Ser	Gln	Asn	Ile	Glu	Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	435	440	445
Trp	Leu	Ala	Glu	Val	Glu	Gly	Arg	Leu	Pro	Ala	Arg	Asn	Glu	Gln	Ala	450	455	460
Arg	Arg	Gln	Ser	Gly	Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	465	470	475
Asn	Cys	Ala	Gln	Asp	Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	485	490	495
Gln	Ser	Gln	Glu	Ser	Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	500	505	510
Glu	Phe	Asp	Asp	Glu	Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	515	520	525
Leu	Tyr	Thr	Phe	Glu	Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu	530	535	540

Cura 468 SEQ list 0405.txt

Gly	Glu	Thr	Leu	Tyr	Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr
545					550					555					560
Arg	Ile	Arg	Arg	Asn	Glu	Asp	Glu	Glu	Gly	Tyr	Val	Pro	Thr	Ser	Tyr
				565					570					575	
Val	Glu	Val	Cys	Leu	Asp	Lys	Asn	Ala	Lys	Gly	Ala	Lys	Thr	Tyr	Ile
			580					585					590		

<210> 69  
 <211> 679  
 <212> PRT  
 <213> Homo sapiens

<400> 69

Leu	Trp	Asn	Gly	Gly	Glu	Glu	Glu	Pro	Pro	Arg	Arg	Pro	Arg	Ala	Arg
1				5					10					15	
Ser	Cys	Glu	Pro	Glu	Glu	Ala	Ala	Arg	Thr	Pro	Gly	Phe	Pro	Pro	Ser
			20					25					30		
Arg	Gly	Ser	Arg	Gly	Ala	Lys	Gly	Ser	Pro	Gly	Arg	Gly	Thr	Arg	Glu
		35					40					45			
Pro	Arg	Pro	Pro	Arg	Gly	Ala	Pro	Leu	Arg	Val	Pro	Cys	Thr	Met	Ser
	50					55					60				
Trp	Gly	Thr	Glu	Leu	Trp	Asp	Gln	Phe	Asp	Asn	Leu	Glu	Lys	His	Thr
65					70					75					80
Gln	Trp	Gly	Ile	Asp	Ile	Leu	Glu	Lys	Tyr	Ile	Lys	Phe	Val	Lys	Glu
				85					90					95	
Arg	Thr	Glu	Ile	Glu	Leu	Ser	Tyr	Ala	Lys	Gln	Leu	Arg	Asn	Leu	Ser
			100					105					110		
Lys	Lys	Tyr	Gln	Pro	Lys	Lys	Asn	Ser	Lys	Glu	Glu	Glu	Glu	Tyr	Lys
		115					120					125			
Tyr	Thr	Ser	Cys	Lys	Ala	Phe	Ile	Ser	Asn	Leu	Asn	Glu	Met	Asn	Asp
	130					135					140				
Tyr	Ala	Gly	Gln	His	Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	Gln	Ile

145					150				155				160			
Ile	Val	Asp	Leu	Ala	Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	Arg	Lys	
				165					170					175		
Ser	Asn	Phe	His	Asp	Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	Thr	Cys	
				180					185					190		
Trp	Lys	Gln	Leu	Glu	Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys	
				195					200					205		
Glu	Ala	Asp	Arg	Ala	Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile	
				210					215					220		
Asn	Val	Thr	Lys	Ala	Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile	
225					230					235					240	
Arg	His	Gln	Met	Ala	Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu	
				245					250					255		
Gln	Lys	Phe	Asn	His	Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro	
				260					265					270		
Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg	
				275					280					285		
Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile	
				290					295					300		
Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser	
305					310					315					320	
Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser	
				325					330					335		
Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro	
				340					345					350		
Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu	
				355					360					365		
Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp	
				370					375					380		
Pro	Phe	Ile	Lys	Lys	Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His	
385					390					395					400	
Gln	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro	

## Cura 468 SEQ list 0405.txt

405																	415
Asn	Gly	Pro	Gln	Ser	Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg		
			420					425					430				
Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser		
		435					440					445					
Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe		
	450						455				460						
Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val		
465					470					475					480		
Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	Asp	Gln	Arg	Asp	Ala		
				485					490					495			
Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	Gly	Asp		
			500					505					510				
Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	Ser	Gln	Asn	Ile	Glu		
		515					520					525					
Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	Glu	Val		
	530					535					540						
Glu	Gly	Arg	Leu	Pro	Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	Ser	Gly		
545					550					555					560		
Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	Asn	Cys	Ala	Gln	Asp		
				565					570					575			
Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	Gln	Ser	Gln	Glu	Ser		
			580					585					590				
Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	Glu	Phe	Asp	Asp	Glu		
		595					600					605					
Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	Leu	Tyr	Thr	Phe	Glu		
	610					615					620						
Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu	Gly	Glu	Thr	Leu	Tyr		
625					630					635					640		
Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ile	Arg	Arg	Asn		
				645					650					655			
Glu	Asp	Glu	Glu	Gly	Tyr	Val	Pro	Thr	Ser	Tyr	Val	Glu	Val	Cys	Leu		

660.

665

670

Asp Lys Asn Ala Lys Asp Ser  
675

&lt;210&gt; 70

&lt;211&gt; 674

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg Ser Cys Glu Pro Glu  
1 5 10 15

Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser Arg Gly Ser Arg Gly  
20 25 30

Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu Pro Arg Pro Pro Arg  
35 40 45

Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser Trp Gly Thr Glu Leu  
50 55 60

Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr Gln Trp Gly Ile Asp  
65 70 75 80

Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu Arg Thr Glu Ile Glu  
85 90 95

Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser Lys Lys Tyr Gln Pro  
100 105 110

Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys Tyr Thr Ser Cys Lys  
115 120 125

Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp Tyr Ala Gly Gln His  
130 135 140

Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile Ile Val Asp Leu Ala  
145 150 155 160

Arg Tyr Val Gln Glu Leu Lys Gln Glu Arg Lys Ser Asn Phe His Asp  
165 170 175

Gly Arg Lys Ala Gln Gln His Ile Glu Thr Cys Trp Lys Gln Leu Glu  
180 185 190

Cura 468 SEQ list 0405.txt

Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys	Glu	Ala	Asp	Arg	Ala		
		195					200					205					
Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile	Asn	Val	Thr	Lys	Ala		
		210				215					220						
Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile	Arg	His	Gln	Met	Ala		
225					230					235					240		
Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu	Gln	Lys	Phe	Asn	His		
				245					250					255			
Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro	Asn	Ile	Phe	Gln	Lys		
			260					265					270				
Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg	Met	Gly	Glu	Ser	Met		
		275					280					285					
Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile	Pro	Ile	Ile	Gly	Lys		
	290					295					300						
Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser	Ile	Asp	Gln	Lys	Asn		
305					310					315					320		
Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser	Gly	Phe	Glu	Pro	Pro		
				325					330					335			
Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro	Met	Lys	Arg	Thr	Val		
			340					345					350				
Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu	Gly	Lys	Pro	Asp	Leu		
		355					360					365					
Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp	Pro	Phe	Ile	Lys	Lys		
	370					375					380						
Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His	Gln	Pro	Pro	Pro	Pro		
385					390					395					400		
Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro	Asn	Gly	Pro	Gln	Ser		
				405					410					415			
Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met		
			420					425					430				
Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu		
		435					440					445					

Cura 468 SEQ list 0405.txt

Ser Leu Lys Leu Gly Ala Thr Pro Glu Asp Phe Ser Asn Leu Pro Pro  
450 455 460

Glu Gln Arg Arg Lys Lys Leu Gln Gln Lys Val Asp Glu Leu Asn Lys  
465 470 475 480

Glu Ile Gln Lys Glu Met Asp Gln Arg Asp Ala Ile Thr Lys Met Lys  
485 490 495

Asp Val Tyr Leu Lys Asn Pro Gln Met Gly Asp Pro Ala Ser Leu Asp  
500 505 510

His Lys Leu Ala Glu Val Ser Gln Asn Ile Glu Lys Leu Arg Val Glu  
515 520 525

Thr Gln Lys Phe Glu Ala Trp Leu Ala Glu Val Glu Gly Arg Leu Pro  
530 535 540

Ala Arg Ser Glu Gln Ala Arg Arg Gln Ser Gly Leu Tyr Asp Ser Gln  
545 550 555 560

Asn Pro Pro Thr Val Asn Asn Cys Ala Gln Asp Arg Glu Ser Pro Asp  
565 570 575

Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser Glu Met Lys Val Leu  
580 585 590

Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu Glu Pro Leu Pro Ala  
595 600 605

Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly  
610 615 620

Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp  
625 630 635 640

Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly  
645 650 655

Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu Asp Lys Asn Ala Lys  
660 665 670

Asp Ser

<210> 71

<211> 457

## Cura 468 SEQ list 0405.txt

<212> PRT

<213> Homo sapiens

<400> 71

Met 1	Ser	Leu	Met	Leu 5	Asp	Asp	Gln	Pro	Pro 10	Met	Glu	Ala	Gln	Tyr 15	Ala
Glu	Glu	Gly	Pro 20	Gly	Pro	Gly	Ile	Phe 25	Arg	Ala	Glu	Pro	Gly 30	Asp	Gln
Gln	His	Pro 35	Ile	Ser	Gln	Ala	Val 40	Cys	Trp	Arg	Ser	Met 45	Arg	Arg	Gly
Cys	Ala 50	Val	Leu	Gly	Ala	Leu 55	Gly	Leu	Leu	Ala	Gly 60	Ala	Gly	Val	Gly
Ser 65	Trp	Leu	Leu	Val	Leu 70	Tyr	Leu	Cys	Pro	Ala 75	Ala	Ser	Gln	Pro	Ile 80
Ser	Gly	Thr	Leu	Gln 85	Asp	Glu	Glu	Ile	Thr 90	Leu	Ser	Cys	Ser	Glu 95	Ala
Ser	Ala	Glu	Glu 100	Ala	Leu	Leu	Pro	Ala 105	Leu	Pro	Lys	Thr	Val 110	Ser	Phe
Arg	Ile	Asn 115	Ser	Glu	Asp	Phe	Leu 120	Leu	Glu	Ala	Gln	Val 125	Arg	Asp	Gln
Pro 130	Arg	Trp	Leu	Leu	Val	Cys 135	His	Glu	Gly	Trp	Ser 140	Pro	Ala	Leu	Gly
Leu 145	Gln	Ile	Cys	Trp	Ser 150	Leu	Gly	His	Leu	Arg 155	Leu	Thr	His	His	Lys 160
Gly	Val	Asn	Leu	Thr 165	Asp	Ile	Lys	Leu	Asn 170	Ser	Ser	Gln	Glu	Phe 175	Ala
Gln	Leu	Ser	Pro 180	Arg	Leu	Gly	Gly	Phe 185	Leu	Glu	Glu	Ala	Trp 190	Gln	Pro
Arg	Asn	Asn 195	Cys	Thr	Ser	Gly	Gln 200	Val	Val	Ser	Leu	Arg 205	Cys	Ser	Glu
Cys	Gly 210	Ala	Arg	Pro	Leu	Ala 215	Ser	Arg	Ile	Val	Gly 220	Gly	Gln	Ser	Val
Ala 225	Pro	Gly	Arg	Trp	Pro 230	Trp	Gln	Ala	Ser	Val 235	Ala	Leu	Gly	Phe	Arg 240



Cura 468 SEQ list 0405.txt

His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala	
				245					250					255		
Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu	Ala	Arg	Leu	Ser	Ser	Trp	Arg	
			260					265					270			
Val	His	Ala	Gly	Leu	Val	Ser	His	Ser	Ala	Val	Arg	Pro	His	Gln	Gly	
		275					280					285				
Ala	Leu	Val	Glu	Arg	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn	
	290					295					300					
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Arg	Leu	Gln	Thr	Ala	Leu	Asn	Phe	
305					310					315					320	
Ser	Asp	Thr	Val	Gly	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	His	Phe	
				325					330					335		
Pro	Lys	Gly	Ser	Arg	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	His	Pro	
			340					345					350			
Ser	His	Thr	Tyr	Ser	Ser	Asp	Met	Leu	Gln	Asp	Thr	Val	Val	Pro	Leu	
		355					360					365				
Phe	Ser	Thr	Gln	Leu	Cys	Asn	Ser	Ser	Cys	Val	Tyr	Ser	Gly	Ala	Leu	
	370					375					380					
Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Asp	Gly	Arg	Ala	Asp	Ala	
385					390					395					400	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Pro	Asp	Gly	Asp	Thr	
				405					410					415		
Trp	Arg	Leu	Val	Gly	Val	Val	Ser	Trp	Gly	Arg	Ala	Cys	Ala	Glu	Pro	
			420					425					430			
Asn	His	Pro	Gly	Val	Tyr	Ala	Lys	Val	Ala	Glu	Phe	Leu	Asp	Trp	Ile	
		435					440					445				
His	Asp	Thr	Ala	Gln	Asp	Ser	Leu	Leu								
	450					455										

<210> 72

<211> 455

<212> PRT

<213> Mus musculus

Cura 468 SEQ list 0405.txt

<400> 72

Met	Ser	Pro	Thr	Leu	Asp	Asp	Gln	Ser	Pro	Met	Glu	Ile	Arg	Cys	Thr
1				5					10					15	
Glu	Glu	Gly	Ala	Gly	Pro	Gly	Ile	Phe	Arg	Met	Glu	Leu	Gly	Asp	Gln
			20					25					30		
Arg	Gln	Ser	Ile	Ser	Gln	Ser	Gln	Arg	Trp	Cys	Cys	Leu	Gln	Arg	Gly
		35					40					45			
Cys	Val	Ile	Leu	Gly	Val	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Ile	Ala
	50					55					60				
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Trp	Pro	Ala	Ala	Ser	Pro	Ser	Ile
65					70					75					80
Ser	Gly	Thr	Leu	Gln	Glu	Glu	Glu	Met	Thr	Leu	Asn	Cys	Pro	Gly	Val
				85					90					95	
Ser	Cys	Glu	Glu	Glu	Leu	Leu	Pro	Ser	Leu	Pro	Lys	Thr	Val	Ser	Phe
			100				105						110		
Arg	Ile	Asn	Gly	Glu	Asp	Leu	Leu	Leu	Gln	Val	Gln	Val	Arg	Ala	Arg
		115					120					125			
Pro	Asp	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly
	130					135					140				
Met	His	Ile	Cys	Lys	Ser	Leu	Gly	His	Ile	Arg	Leu	Thr	Gln	His	Lys
145					150					155					160
Ala	Val	Asn	Leu	Ser	Asp	Ile	Lys	Leu	Asn	Arg	Ser	Gln	Glu	Phe	Ala
				165					170					175	
Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val	Glu	Glu	Ala	Trp	Lys	Pro
			180					185					190		
Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val	Ser	Leu	Lys	Cys	Ser	Glu
		195					200					205			
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ala	Val
	210					215					220				
Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Met	Leu	Gly	Ser	Arg
225					230					235					240
His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro	His	Trp	Val	Val	Thr	Ala

## Cura 468 SEQ list 0405.txt

245

250

255

Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser	Arg	Leu	Ser	Ser	Trp	Arg
			260					265					270		
Val	His	Ala	Gly	Leu	Val	Ser	His	Gly	Ala	Val	Arg	Gln	His	Gln	Gly
		275					280					285			
Thr	Met	Val	Glu	Lys	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn
	290					295					300				
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu	Arg	Thr	Pro	Ile	Asn	Phe
305					310					315					320
Ser	Asp	Thr	Val	Asp	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	Tyr	Phe
				325					330					335	
Pro	Trp	Gly	Ser	Gln	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	Asp	Pro
			340					345						350	
Ser	His	Thr	His	Ser	Ser	Asp	Thr	Leu	Gln	Asp	Thr	Met	Val	Pro	Leu
		355					360					365			
Leu	Ser	Thr	His	Leu	Cys	Asn	Ser	Ser	Cys	Met	Tyr	Ser	Gly	Ala	Leu
	370					375					380				
Thr	His	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Asp	Gly	Arg	Ala	Asp	Ala
385					390					395					400
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Pro	Ser	Gly	Asp	Thr
				405					410					415	
Trp	His	Leu	Val	Gly	Val	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Glu	Pro
			420					425					430		
Asn	Arg	Pro	Gly	Val	Tyr	Ala	Lys	Val	Ala	Glu	Phe	Leu	Asp	Trp	Ile
		435					440					445			
His	Asp	Thr	Val	Gln	Val	Arg									
	450					455									

&lt;210&gt; 73

&lt;211&gt; 445

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 73

Cura 468 SEQ list 0405.txt

Met	Glu	Ile	Arg	Cys	Thr	Glu	Glu	Gly	Ala	Gly	Pro	Gly	Ile	Phe	Arg	1	5	10	15
Met	Glu	Leu	Gly	Asp	Gln	Arg	Gln	Ser	Ile	Ser	Gln	Ser	Gln	Arg	Trp	20	25	30	
Cys	Cys	Leu	Gln	Arg	Gly	Cys	Val	Ile	Leu	Gly	Val	Leu	Gly	Leu	Leu	35	40	45	
Ala	Gly	Ala	Gly	Ile	Ala	Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Trp	Pro	50	55	60	
Ala	Ala	Ser	Pro	Ser	Ile	Ser	Gly	Thr	Leu	Gln	Glu	Glu	Glu	Met	Thr	65	70	75	
Leu	Asn	Cys	Pro	Gly	Val	Ser	Cys	Glu	Glu	Glu	Leu	Leu	Pro	Ser	Leu	85	90	95	
Pro	Lys	Thr	Val	Ser	Phe	Arg	Ile	Asn	Gly	Glu	Asp	Leu	Leu	Leu	Gln	100	105	110	
Val	Gln	Val	Arg	Ala	Arg	Pro	Asp	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	115	120	125	
Trp	Ser	Pro	Ala	Leu	Gly	Met	His	Ile	Cys	Lys	Ser	Leu	Gly	His	Ile	130	135	140	
Arg	Leu	Thr	Gln	His	Lys	Ala	Val	Asn	Leu	Ser	Asp	Ile	Lys	Leu	Asn	145	150	155	
Arg	Ser	Gln	Glu	Phe	Ala	Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val	165	170	175	
Glu	Glu	Ala	Trp	Lys	Pro	Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val	180	185	190	
Ser	Leu	Lys	Cys	Ser	Glu	Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	195	200	205	
Val	Gly	Gly	Gln	Ala	Val	Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	210	215	220	
Val	Met	Leu	Gly	Ser	Arg	His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro	225	230	235	
His	Trp	Val	Val	Thr	Ala	Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser	245	250	255	

Cura 468 SEQ list 0405.txt

Arg	Leu	Ser	Ser	Trp	Arg	Val	His	Ala	Gly	Leu	Val	Ser	His	Gly	Ala
			260					265					270		
Val	Arg	Gln	His	Gln	Gly	Thr	Met	Val	Glu	Lys	Ile	Ile	Pro	His	Pro
		275					280					285			
Leu	Tyr	Ser	Ala	Gln	Asn	His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu
	290					295					300				
Arg	Thr	Pro	Ile	Asn	Phe	Ser	Asp	Thr	Val	Gly	Ala	Val	Cys	Leu	Pro
305					310					315					320
Ala	Lys	Glu	Gln	Tyr	Phe	Pro	Trp	Gly	Ser	Gln	Cys	Trp	Val	Ser	Gly
				325					330					335	
Trp	Gly	His	Thr	Asp	Pro	Ser	His	Thr	His	Ser	Ser	Asp	Thr	Leu	Gln
			340					345					350		
Asp	Thr	Met	Val	Pro	Leu	Leu	Ser	Thr	His	Leu	Cys	Asn	Ser	Ser	Cys
		355					360					365			
Met	Tyr	Ser	Gly	Ala	Leu	Thr	His	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Leu
	370					375					380				
Asp	Gly	Arg	Ala	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val
385					390					395					400
Cys	Pro	Ser	Gly	Asp	Thr	Trp	His	Leu	Val	Gly	Val	Val	Ser	Trp	Gly
				405					410					415	
Arg	Gly	Cys	Ala	Glu	Pro	Asn	Arg	Pro	Gly	Val	Tyr	Ala	Lys	Val	Ala
			420					425					430		
Glu	Phe	Leu	Asp	Trp	Ile	His	Asp	Thr	Val	Gln	Val	Arg			
		435					440					445			

<210> 74

<211> 398

<212> PRT

<213> Homo sapiens

<400> 74

Met	Ser	Leu	Met	Leu	Asp	Asp	Gln	Pro	Pro	Met	Glu	Ala	Gln	Tyr	Ala
1				5					10					15	

Glu	Glu	Gly	Pro	Gly	Pro	Gly	Ile	Phe	Arg	Ala	Glu	Pro	Gly	Asp	Gln
			20					25					30		

Cura 468 SEQ list 0405.txt

Gln	His	Pro	Ile	Ser	Gln	Ala	Val	Cys	Trp	Arg	Ser	Met	Arg	Arg	Gly			
		35					40					45						
Cys	Ala	Val	Leu	Gly	Ala	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Val	Gly			
	50					55					60							
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Cys	Pro	Ala	Ala	Ser	Gln	Pro	Ile			
65					70					75					80			
Ser	Gly	Thr	Leu	Gln	Asp	Glu	Glu	Ile	Thr	Leu	Ser	Cys	Ser	Glu	Ala			
				85					90					95				
Ser	Ala	Glu	Glu	Ala	Leu	Leu	Pro	Ala	Leu	Pro	Lys	Thr	Val	Ser	Phe			
			100					105					110					
Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln			
		115					120					125						
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly			
	130					135					140							
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys			
145					150					155					160			
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala			
				165					170					175				
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro			
			180					185					190					
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu			
		195					200					205						
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val			
	210					215					220							
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg			
225					230					235					240			
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala			
				245					250					255				
Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu	Ala	Arg	Leu	Ser	Ser	Trp	Arg			
			260					265					270					
Val	His	Ala	Gly	Leu	Val	Ser	His	Ser	Ala	Val	Arg	Pro	His	Gln	Gly			
		275					280					285						

Cura 468 SEQ list 0405.txt

Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn  
 290 295 300

His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe  
 305 310 315 320

Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe  
 325 330 335

Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro  
 340 345 350

Ser His Ser Leu Gln Leu Gly Tyr Ala Pro Gly His Gly Gly Ala Leu  
 355 360 365

Val Gln His Ser Ala Leu Gln Gln Leu Leu Arg Val Gln Arg Ser Pro  
 370 375 380

His Pro Pro His Ala Leu Arg Trp Leu Pro Gly Arg Lys Gly  
 385 390 395

<210> 75

<211> 311

<212> PRT

<213> Mus musculus

<400> 75

Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys  
 1 5 10 15

Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala  
 20 25 30

Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro  
 35 40 45

Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu  
 50 55 60

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val  
 65 70 75 80

Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg  
 85 90 95

His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala

## Cura 468 SEQ list 0405.txt

100

105

110

Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg  
 115 . 120 125

Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly  
 130 135 140

Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn  
 145 150 155 160

His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe  
 165 170 175

Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe  
 180 185 190

Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro  
 195 200 205

Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu  
 210 215 220

Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu  
 225 230 235 240

Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala  
 245 250 255

Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr  
 260 265 270

Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro  
 275 280 285

Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile  
 290 295 300

His Asp Thr Val Gln Val Arg  
 305 310

&lt;210&gt; 76

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;



<223> Description of Artificial Sequence: Reprolysin  
family zinc protease Consensus Sequence

&lt;400&gt; 76

Lys	Tyr	Ile	Glu	Leu	Phe	Ile	Val	Val	Asp	His	Gly	Met	Phe	Thr	Lys
1				5					10					15	

Tyr	Gly	Ser	Asp	Leu	Asn	Lys	Ile	Arg	Gln	Arg	Val	His	Gln	Ile	Val
			20					25					30		

Asn	Leu	Val	Asn	Glu	Ile	Tyr	Arg	Pro	Leu	Asn	Ile	Arg	Val	Val	Leu
		35					40					45			

Val	Gly	Leu	Glu	Ile	Trp	Ser	Asp	Gly	Asp	Lys	Ile	Thr	Val	Gln	Gly
	50					55					60				

Asp	Ala	Asn	Asp	Thr	Leu	His	Arg	Phe	Leu	Glu	Trp	Arg	Glu	Thr	Asp
65					70					75					80

Leu	Leu	Lys	Arg	Lys	Ser	His	Asp	Asn	Ala	Gln	Leu	Leu	Thr	Gly	Ile
				85					90					95	

Asp	Phe	Asp	Gly	Asn	Thr	Ile	Gly	Ala	Ala	Tyr	Val	Gly	Gly	Met	Cys
			100					105					110		

Ser	Pro	Lys	Arg	Ser	Val	Gly	Val	Val	Gln	Asp	His	Ser	Pro	Ile	Val
		115					120					125			

Leu	Leu	Val	Ala	Val	Thr	Met	Ala	His	Glu	Leu	Gly	His	Asn	Leu	Gly
	130					135					140				

Met	Thr	His	Asp	Asp	Ile	Asn	Lys	Cys	Thr	Cys	Glu	Gly	Gly	Gly	Gly
145					150					155					160

Cys	Ile	Met	Asn	Pro	Val	Ala	Ser	Ser	Ser	Pro	Gly	Lys	Lys	Phe	Ser
				165					170					175	

Asn	Cys	Ser	Met	Asp	Asp	Tyr	Gln	Gln	Phe	Leu	Thr	Lys	Gly	Lys	Pro
			180					185					190		

Gln	Cys	Leu	Leu	Asn	Lys	Pro
		195				

&lt;210&gt; 77

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thrombospondin  
type 1 Consensus Sequence

<400> 77

Trp Gly Glu Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Gly  
1 5 10 15

Gly Val Gln Thr Arg Thr Arg Cys Cys Asn Pro Pro Pro Asn Gly Gly  
20 25 30

Gly Pro Cys Thr Gly Pro Asp Thr Glu Thr Arg Ala Cys Asn Glu Gln  
35 40 45

Pro Cys Pro  
50

<210> 78

<211> 48

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thrombospondin  
type 1 domain Consensus Sequence

<400> 78

Ser Pro Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Lys Gly  
1 5 10 15

Ile Arg Thr Arg Gln Arg Thr Cys Asn Ser Pro Ala Gly Gly Lys Pro  
20 25 30

Cys Thr Gly Asp Ala Gln Glu Thr Glu Ala Cys Met Met Asp Pro Cys  
35 40 45

<210> 79

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reprolysin  
family propeptide Consensus Sequence

<400> 79

```

His Leu Glu Lys Asn Arg Ser Leu Leu Ala Pro Asp Phe Thr Val Thr
 1              5              10              15

Thr Tyr Asp Asp Asp Gly Thr Leu Val Thr Glu His Pro Leu Ile Gln
              20              25              30

Asp His Cys Tyr Tyr Gln Gly Tyr Val Glu Gly Tyr Pro Asn Ser Ala
              35              40              45

Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Leu Glu
 50              55              60

Asn Leu Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ser Asp Gly Phe Glu
 65              70              75              80

His Ile Ile Tyr Gln Ile Glu His Leu Lys Thr Val Pro Gly Pro Cys
              85              90              95

Gly Glu Cys Gly Ser Leu Ser Val Ser Thr Asp Ser Gln Tyr Gly Ile
              100              105              110

Arg Ser Pro Ser Pro
      115
    
```

<210> 80

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Alpha-2-macroglobulin family Consensus Sequence

<400> 80

```

Ile Asp Glu Asp Asp Ile Thr Ile Arg Ser Tyr Phe Pro Glu Ser Trp
 1              5              10              15

Leu Trp Glu Val Glu Glu Val Asp Arg Ser Pro Val Leu Thr Val Asn
              20              25              30

Ile Thr Leu Pro Asp Ser Ile Thr Thr Trp Glu Ile Leu Ala Val Ser
 35              40              45
    
```

Cura 468 SEQ list 0405.txt

Leu	Ser	Asn	Thr	Lys	Gly	Leu	Cys	Val	Ala	Asp	Pro	Val	Glu	Leu	Thr
	50					55					60				
Val	Phe	Gln	Asp	Phe	Phe	Leu	Glu	Leu	Arg	Leu	Pro	Tyr	Ser	Val	Val
65					70					75					80
Arg	Gly	Glu	Gln	Val	Glu	Leu	Arg	Ala	Val	Leu	Tyr	Asn	Tyr	Leu	Pro
				85					90					95	
Ser	Gln	Asp	Ile	Lys	Val	Val	Val	Gln	Leu	Glu	Val	Glu	Pro	Leu	Cys
			100					105					110		
Gln	Ala	Gly	Phe	Cys	Ser	Leu	Ala	Thr	Gln	Arg	Thr	Arg	Ser	Ser	Gln
		115					120					125			
Ser	Val	Arg	Pro	Lys	Ser	Leu	Ser	Ser	Val	Ser	Phe	Pro	Val	Val	Val
	130					135					140				
Val	Pro	Leu	Ala	Ser	Gly	Leu	Ser	Leu	Val	Glu	Val	Val	Ala	Ser	Val
145					150					155					160
Pro	Glu	Phe	Phe	Val	Lys	Asp	Ala	Val	Val	Lys	Thr	Leu	Lys	Val	Glu
				165					170					175	
Pro	Glu	Gly	Ala	Arg	Lys	Glu	Glu	Thr	Val	Ser	Ser	Leu	Leu	Leu	Pro
			180					185					190		
Pro	Glu	His	Leu	Gly	Gly	Gly	Leu	Glu	Val	Ser	Glu	Val	Pro	Ala	Leu
		195					200					205			
Lys	Leu	Pro	Asp	Asp	Val	Pro	Asp	Thr	Glu	Ala	Glu	Ala	Val	Ile	Ser
	210					215					220				
Val	Gln	Gly	Asp	Pro	Val	Ala	Gln	Ala	Ile	Gln	Asn	Thr	Leu	Ser	Gly
225					230					235					240
Glu	Gly	Leu	Asn	Asn	Leu	Leu	Arg	Leu	Pro	Ser	Gly	Cys	Gly	Glu	Gln
				245					250					255	
Asn	Met	Ile	Tyr	Met	Ala	Pro	Thr	Val	Tyr	Val	Leu	His	Tyr	Leu	Asp
			260					265					270		
Glu	Thr	Trp	Gln	Trp	Glu	Lys	Pro	Gly	Thr	Lys	Lys	Lys	Gln	Lys	Ala
		275					280						285		
Ile	Asp	Leu	Ile	Asn	Lys	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Arg	Lys
	290					295					300				

Cura 468 SEQ list 0405.txt

Ala	Asp	Gly	Ser	Tyr	Ala	Ala	Phe	Leu	His	Arg	Ala	Ser	Ser	Thr	Trp
305					310					315					320
Leu	Thr	Ala	Phe	Val	Leu	Lys	Val	Phe	Ser	Gln	Ala	Arg	Asn	Tyr	Val
				325					330					335	
Phe	Ile	Asp	Glu	Glu	His	Ile	Cys	Gly	Ala	Val	Lys	Trp	Leu	Ile	Leu
			340					345					350		
Asn	Gln	Gln	Lys	Asp	Asp	Gly	Val	Phe	Arg	Glu	Ser	Gly	Pro	Val	Ile
		355					360					365			
His	Asn	Glu	Met	Lys	Gly	Gly	Val	Gly	Asp	Asp	Ala	Glu	Val	Glu	Val
	370					375					380				
Thr	Leu	Thr	Ala	Phe	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ala	Lys	Leu	Val
385					390					395					400
Cys	Ile	Ser	Pro	Val	Val	Ala	Asn	Ala	Leu	Ser	Ile	Leu	Lys	Ala	Ser
				405					410					415	
Asp	Tyr	Leu	Leu	Glu	Asn	Tyr	Ala	Asn	Gly	Gln	Arg	Val	Tyr	Thr	Leu
			420					425					430		
Ala	Leu	Thr	Ala	Tyr	Ala	Leu	Ala	Leu	Ala	Gly	Val	Leu	His	Lys	Leu
		435					440					445			
Lys	Glu	Ile	Leu	Lys	Ser	Leu	Lys	Glu	Glu	Leu	Tyr	Lys	Ala	Leu	Val
	450					455					460				
Lys	Gly	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Asp	Ala	Pro	Gly	His
465					470					475					480
Pro	Tyr	Ser	Pro	Gln	Pro	Gln	Ala	Ala	Ala	Val	Glu	Met	Thr	Ser	Tyr
				485					490					495	
Ala	Leu	Leu	Ala	Leu	Leu	Thr	Leu	Leu	Pro	Phe	Pro	Lys	Val	Glu	Met
			500					505					510		
Ala	Pro	Lys	Val	Val	Lys	Trp	Leu	Thr	Glu	Gln	Gln	Tyr	Tyr	Gly	Gly
		515					520					525			
Gly	Phe	Gly	Ser	Thr	Gln	Asp	Thr	Val	Met	Ala	Leu	Gln	Ala	Leu	Ser
	530					535					540				
Lys	Tyr	Gly	Ile	Ala	Thr	Pro	Thr	His	Lys	Glu	Lys	Asn	Leu	Ser	Val
545					550					555					560

Cura 468 SEQ list 0405.txt

Thr	Ile	Gln	Ser	Pro	Ser	Gly	Ser	Phe	Lys	Ser	His	Phe	Gln	Ile	Leu
				565					570					575	
Asn	Asn	Asn	Ala	Phe	Leu	Leu	Arg	Pro	Val	Glu	Leu	Pro	Leu	Asn	Glu
			580					585					590		
Gly	Phe	Thr	Val	Thr	Ala	Lys	Val	Thr	Gly	Gln	Gly	Thr	Leu	Thr	Leu
		595					600					605			
Val	Thr	Thr	Tyr	Arg	Tyr	Lys	Val	Leu	Asp	Lys	Lys	Asn	Thr	Phe	Cys
	610					615					620				
Phe	Asp	Leu	Lys	Ile	Glu	Thr	Val	Pro	Asp	Thr	Cys	Val	Glu	Pro	Lys
625					630					635					640
Gly	Ala	Lys	Asn	Ser	Asp	Tyr	Leu	Ser	Ile	Cys	Thr	Arg	Tyr	Ala	Gly
			645						650					655	
Ser	Arg	Ser	Asp	Ser	Gly	Met	Ala	Ile	Ala	Asp	Ile	Ser	Met	Leu	Thr
			660					665					670		
Gly	Phe	Ile	Pro	Leu	Lys	Pro	Asp	Leu	Lys	Lys	Leu	Glu	Asn	Gly	Val
		675					680					685			
Asp	Arg	Tyr	Val	Ser	Lys	Tyr	Glu	Ile	Asp	Gly	Asn	His	Val	Leu	Leu
	690					695					700				
Tyr	Leu	Asp	Lys	Val	Ser	His	Ser	Glu	Thr	Glu	Cys	Val	Gly	Phe	Lys
705					710					715					720
Ile	His	Gln	Asp	Phe	Glu	Val	Gly	Leu	Leu	Gln	Pro	Ala	Ser	Val	Lys
			725						730					735	
Val	Tyr	Asp	Tyr	Tyr	Glu	Pro	Asp	Glu	Gln	Cys	Thr	Ala	Phe	Tyr	
			740					745					750		

<210> 81

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Alpha-2-macroglobulin family N-terminal region  
Consensus Sequence

<400> 81

Cura 468 SEQ list 0405.txt

Arg	Leu	Leu	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Phe	Asp	Ser	Ser		
1				5					10					15			
Leu	Gln	Lys	Pro	Arg	Tyr	Met	Val	Ile	Val	Pro	Ser	Ile	Leu	Arg	Thr		
			20					25					30				
Glu	Thr	Pro	Glu	Lys	Val	Cys	Val	Gln	Leu	His	Asp	Leu	Asn	Glu	Thr		
		35					40					45					
Val	Thr	Val	Thr	Val	Ser	Leu	His	Ser	Phe	Pro	Gly	Lys	Arg	Asn	Leu		
	50					55					60						
Ser	Ser	Leu	Phe	Thr	Val	Leu	Leu	Ser	Ser	Lys	Asp	Leu	Phe	His	Cys		
65					70					75					80		
Val	Ser	Phe	Thr	Val	Pro	Gln	Pro	Gly	Leu	Phe	Lys	Ser	Ser	Lys	Gly		
				85					90					95			
Glu	Glu	Ser	Phe	Val	Val	Val	Gln	Val	Lys	Gly	Pro	Thr	His	Thr	Phe		
			100					105					110				
Lys	Glu	Lys	Val	Thr	Val	Leu	Val	Ser	Ser	Arg	Arg	Gly	Leu	Val	Phe		
		115					120					125					
Ile	Gln	Thr	Asp	Lys	Pro	Ile	Tyr	Thr	Pro	Gly	Gln	Thr	Val	Arg	Tyr		
	130					135					140						
Arg	Val	Phe	Ser	Val	Asp	Glu	Asn	Leu	Arg	Pro	Leu	Asn	Glu	Leu	Ile		
145					150					155					160		
Leu	Val	Tyr	Ile	Glu	Asp	Pro	Glu	Gly	Asn	Arg	Val	Asp	Gln	Trp	Glu		
				165					170					175			
Val	Asn	Lys	Leu	Glu	Gly	Gly	Ile	Phe	Gln	Leu	Ser	Phe	Pro	Ile	Pro		
			180					185					190				
Ser	Glu	Pro	Ile	Gln	Gly	Thr	Trp	Lys	Ile	Val	Ala	Arg	Tyr	Glu	Ser		
		195					200					205					
Gly	Pro	Glu	Ser	Asn	Tyr	Thr	His	Tyr	Phe	Glu	Val	Lys	Glu	Tyr	Val		
	210					215					220						
Leu	Pro	Ser	Phe	Glu	Val	Ser	Ile	Thr	Pro	Pro	Lys	Pro	Phe	Ile	Tyr		
225					230					235					240		
Tyr	Asp	Asn	Phe	Lys	Glu	Phe	Glu	Val	Thr	Ile	Cys	Ala	Arg	Tyr	Thr		
				245					250					255			

Cura 468 SEQ list 0405.txt

Tyr	Gly	Lys	Pro	Val	Pro	Gly	Val	Ala	Tyr	Val	Arg	Phe	Gly	Val	Lys	260	265	270
Asp	Glu	Asp	Gly	Lys	Lys	Glu	Leu	Leu	Ala	Gly	Leu	Glu	Glu	Arg	Ala	275	280	285
Lys	Leu	Leu	Asp	Gly	Asn	Gly	Glu	Ile	Cys	Leu	Ser	Gln	Glu	Val	Leu	290	295	300
Leu	Lys	Glu	Leu	Gln	Leu	Lys	Asn	Glu	Asp	Leu	Glu	Gly	Lys	Ser	Leu	305	310	315
Tyr	Val	Ala	Val	Ala	Val	Ile	Glu	Ser	Glu	Gly	Gly	Asp	Met	Glu	Glu	325	330	335
Ala	Glu	Leu	Gly	Gly	Ile	Lys	Ile	Val	Arg	Ser	Pro	Tyr	Lys	Leu	Lys	340	345	350
Phe	Val	Lys	Thr	Pro	Ser	His	Phe	Lys	Pro	Gly	Ile	Pro	Phe	Phe	Leu	355	360	365
Lys	Val	Leu	Val	Val	Asp	Pro	Asp	Gly	Ser	Pro	Ala	Pro	Asn	Val	Pro	370	375	380
Val	Lys	Val	Ser	Ala	Gln	Asp	Ala	Ser	Tyr	Tyr	Ser	Asn	Gly	Thr	Thr	385	390	395
Asp	Glu	Asp	Gly	Leu	Ala	Gln	Phe	Ser	Ile	Asn	Thr	Ser	Gly	Ile	Ser	405	410	415
Ser	Leu	Ser	Ile	Thr	Val	Arg	Thr	Asn	His	Lys	Glu	Leu	Pro	Glu	Glu	420	425	430
Val	Gln	Ala	His	Ala	Glu	Ala	Gln	Ala	Thr	Ala	Tyr	Ser	Thr	Val	Ser	435	440	445
Leu	Ser	Lys	Ser	Tyr	Ile	His	Leu	Ser	Ile	Glu	Arg	Thr	Leu	Pro	Cys	450	455	460
Gly	Pro	Gly	Val	Gly	Glu	Gln	Ala	Asn	Phe	Ile	Leu	Arg	Gly	Lys	Ser	465	470	475
Leu	Gly	Glu	Leu	Lys	Ile	Leu	His	Phe	Tyr	Tyr	Leu	Ile	Met	Ser	Lys	485	490	495
Gly	Lys	Ile	Val	Lys	Thr	Gly	Arg	Glu	Pro	Arg	Glu	Pro	Gly	Gln	Gly	500	505	510



Cura 468 SEQ list 0405.txt

Leu Phe Ser Leu Ser Ile Pro Val Thr Pro Asp Leu Ala Pro Ser Phe  
515 520 525

Arg Leu Val Ala Tyr Tyr Ile Leu Pro Gln Gly Glu Val Val Ala Asp  
530 535 540

Ser Val Trp Ile Asp Val Glu Asp Cys Cys Ala Asn Lys Leu Asp Leu  
545 550 555 560

Ser Phe Ser Pro Ser Lys Asp Tyr Arg Leu Pro Ala Gln Gln Val Lys  
565 570 575

Leu Arg Val Glu Ala Asp Pro Gln Ser Leu Val Ala Leu Arg Ala Val  
580 585 590

Asp Gln Ala Val Tyr Leu Leu Lys Pro Lys Ala Lys Leu Ser Met Ser  
595 600 605

Lys Val Tyr Asp Leu Leu Glu Lys Ser Asp Leu Gly  
610 615 620

<210> 82

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sodium Bile  
acid symporter family consensus sequence

<400> 82

Ala Leu Gly Leu Phe Leu Met Met Phe Ser Met Gly Leu Lys Val Arg  
1 5 10 15

Phe Glu Asp Leu Lys Glu Ala Leu Arg Arg Pro Lys Ala Leu Ile Leu  
20 25 30

Gly Leu Leu Leu Gln Trp Ile Ile Met Pro Leu Leu Met Phe Ile Leu  
35 40 45

Ala Trp Leu Leu Leu Arg Leu Pro Pro Glu Leu Ala Thr Gly Leu Ile  
50 55 60

Leu Val Gly Cys Ala Pro Gly Gly Ala Met Ser Asn Val Trp Thr Tyr  
65 70 75 80

Leu Ala Lys Gly Asp Val Glu Leu Ser Val Val Met Val Ala Leu Ser

Cura 468 SEQ list 0405.txt

85

90

95

Thr Leu Leu Ala Pro Leu Val Thr Pro Leu Leu Ser Phe Leu Leu Ala  
100 105 110

Gly Leu Leu Val His Val Asp Ala Val Ser Pro Trp Ser Leu Ile Lys  
115 120 125

Ser Val Leu Val Tyr Val Ile Ile Pro Leu Ile Ala Gly Met Leu Thr  
130 135 140

Arg Tyr Phe Leu Pro Glu Trp Phe Glu Gln Arg Val Leu Pro Val Leu  
145 150 155 160

Ser Pro Ile Ser Leu Ile Gly Leu Leu Leu Thr Ile Val Val Ile Phe  
165 170 175

Ala Leu Asn Gly Glu Val Ile Ala Ser Leu  
180 185

<210> 83

<211> 191

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SPFH  
domain/Band 7 family Consensus Sequence

<400> 83

Val Ala Leu Leu Ile Ile Ile Ala Leu Val Val Ile Ala Met Ser Val  
1 5 10 15

Lys Ile Val Lys Glu Tyr Glu Arg Gly Val Ile Phe Arg Leu Gly Arg  
20 25 30

Tyr Val Arg Gln Val Val Gly Pro Gly Leu His Phe Ile Ile Pro Phe  
35 40 45

Ile Asp Thr Val Lys Lys Val Asp Leu Arg Thr Val Val Tyr Asp Val  
50 55 60

Pro Ser Gln Glu Ile Ile Thr Lys Asp Asn Val Val Val Ile Val Asp  
65 70 75 80

Ala Val Val Tyr Tyr Arg Val Val Asp Pro Leu Lys Ala Val Tyr Glu  
85 90 95

Cura 468 SEQ list 0405.txt

Val	Glu	Asp	Ala	Glu	Arg	Ala	Leu	Pro	Gln	Leu	Ala	Gln	Thr	Thr	Leu
			100					105					110		
Arg	Asn	Val	Ile	Gly	Gln	Phe	Thr	Leu	Asp	Glu	Ile	Leu	Thr	Glu	Arg
		115					120					125			
Glu	Arg	Ile	Asn	Ser	Gln	Leu	Arg	Glu	Ile	Leu	Asp	Glu	Ala	Thr	Asp
		130				135					140				
Pro	Trp	Gly	Ile	Lys	Val	Glu	Arg	Val	Glu	Ile	Lys	Asp	Ile	Arg	Leu
145					150					155					160
Pro	Glu	Glu	Val	Gln	Arg	Ala	Met	Ala	Ala	Gln	Met	Glu	Ala	Glu	Arg
				165					170					175	
Glu	Ala	Arg	Ala	Lys	Ile	Leu	Glu	Ala	Glu	Gly	Glu	Gln	Glu	Ala	
			180					185					190		

<210> 84

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Prohibitin  
homologues Consensus Sequence

<400> 84

Ala	Ala	Phe	Tyr	Val	Ile	Gly	Glu	Gly	Glu	Arg	Gly	Val	Val	Glu	Arg
1				5					10					15	
Leu	Gly	Arg	Val	Leu	Lys	Val	Leu	Gly	Pro	Gly	Leu	His	Phe	Val	Ile
			20					25					30		
Pro	Phe	Ile	Asp	Asp	Val	Lys	Arg	Val	Asp	Leu	Arg	Ala	Gln	Thr	Asp
			35				40					45			
Asp	Val	Pro	Pro	Gln	Glu	Val	Ile	Thr	Lys	Asp	Asn	Val	Thr	Val	Ser
			50			55					60				
Val	Asp	Ala	Val	Val	Tyr	Tyr	Arg	Val	Leu	Asp	Pro	Leu	Lys	Ala	Val
	65				70					75					80
Tyr	Gly	Val	Leu	Asp	Ala	Asp	Tyr	Arg	Ala	Leu	Arg	Gln	Leu	Ala	Gln
				85					90						95

Cura 468 SEQ list 0405.txt

Thr	Thr	Leu	Arg	Ser	Val	Ile	Gly	Lys	Arg	Thr	Leu	Asp	Glu	Leu	Leu
			100					105					110		
Thr	Asp	Glu	Arg	Glu	Lys	Ile	Ser	Glu	Asn	Ile	Arg	Glu	Glu	Leu	Asn
		115					120					125			
Glu	Ala	Ala	Glu	Pro	Trp	Gly	Ile	Glu	Val	Glu	Asp	Val	Glu	Ile	Lys
		130				135					140				
Asp	Ile	Arg	Leu	Pro	Glu	Glu	Ile	Lys	Glu	Ala	Met	Glu	Ala	Gln	Gln
145					150					155					160

<210> 85  
 <211> 79  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Kringle domain  
 Consensus Sequence

<400> 85															
Cys	Tyr	His	Gly	Asn	Gly	Glu	Asn	Tyr	Arg	Gly	Thr	Ala	Ser	Thr	Thr
1				5					10					15	
Glu	Ser	Gly	Ala	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Thr	Pro	His	Arg
			20					25					30		
His	Ser	Lys	Tyr	Thr	Pro	Glu	Arg	Tyr	Pro	Ala	Lys	Gly	Leu	Gly	Glu
		35					40					45			
Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Glu	Arg	Pro	Trp	Cys	Tyr	Thr
	50					55					60				
Thr	Asp	Pro	Arg	Val	Arg	Trp	Glu	Tyr	Cys	Asp	Ile	Pro	Arg	Cys	
65					70					75					

<210> 86  
 <211> 83  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Kringle domain  
Consensus Sequence

<400> 86

Arg	Asp	Cys	Tyr	Ala	Gly	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	Thr	Ala	Ser
1				5					10					15	
Thr	Thr	Lys	Ser	Gly	Lys	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Thr	Pro
			20					25					30		
His	Leu	His	Arg	Phe	Thr	Pro	Glu	Arg	Phe	Pro	Glu	Leu	Gly	Leu	Glu
		35					40					45			
His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	Glu	Gly	Pro	Trp	Cys
	50					55					60				
Tyr	Thr	Thr	Asp	Pro	Asn	Val	Arg	Trp	Glu	Tyr	Cys	Asp	Ile	Pro	Gln
65					70					75					80
Cys Glu Ser															

<210> 87

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like  
serine protease Consensus Sequence

<400> 87

Arg	Ile	Val	Gly	Gly	Ser	Glu	Ala	Asn	Ile	Gly	Ser	Phe	Pro	Trp	Gln
1				5					10					15	
Val	Ser	Leu	Gln	Tyr	Arg	Gly	Gly	Arg	His	Phe	Cys	Gly	Gly	Ser	Leu
			20					25					30		
Ile	Ser	Pro	Arg	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Val	Tyr	Gly	Ser
		35					40				45				
Ala	Pro	Ser	Ser	Ile	Arg	Val	Arg	Leu	Gly	Ser	His	Asp	Leu	Ser	Ser
	50					55					60				
Gly	Glu	Glu	Thr	Gln	Thr	Val	Lys	Val	Ser	Lys	Val	Ile	Val	His	Pro
65					70					75					80

Cura 468 SEQ list 0405.txt

Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu  
85 90 95

Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro  
100 105 110

Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly  
115 120 125

Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln  
130 135 140

Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr  
145 150 155 160

Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu  
165 170 175

Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val  
180 185 190

Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser  
195 200 205

Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser  
210 215 220

Ser Tyr Leu Asp Trp Ile  
225 230

<210> 88

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin  
Consensus Sequence

<400> 88

Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val  
1 5 10 15

Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser  
20 25 30

Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser

Cura 468 SEQ list 0405.txt

35

40

45

Val	Arg	Val	Val	Leu	Gly	Glu	His	Asn	Leu	Gly	Thr	Thr	Glu	Gly	Thr
50					55					60					
Glu	Gln	Lys	Phe	Asp	Val	Lys	Lys	Ile	Ile	Val	His	Pro	Asn	Tyr	Asn
65					70					75					80
Pro	Asp	Thr	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Leu	Lys	Ser	Pro	Val	Thr
				85					90					95	
Leu	Gly	Asp	Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro	Ser	Ala	Ser	Ser	Asp
			100					105					110		
Leu	Pro	Val	Gly	Thr	Thr	Cys	Ser	Val	Ser	Gly	Trp	Gly	Arg	Thr	Lys
		115					120					125			
Asn	Leu	Gly	Thr	Ser	Asp	Thr	Leu	Gln	Glu	Val	Val	Val	Pro	Ile	Val
		130				135						140			
Ser	Arg	Glu	Thr	Cys	Arg	Ser	Ala	Tyr	Gly	Gly	Thr	Val	Thr	Asp	Thr
145					150					155					160
Met	Ile	Cys	Ala	Gly	Ala	Leu	Gly	Gly	Lys	Asp	Ala	Cys	Gln	Gly	Asp
				165					170					175	
Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Asp	Gly	Glu	Leu	Val	Gly	Ile	Val
			180					185					190		
Ser	Trp	Gly	Tyr	Gly	Cys	Ala	Val	Gly	Asn	Tyr	Pro	Gly	Val	Tyr	Thr
		195					200					205			
Arg	Val	Ser	Arg	Tyr	Leu	Asp	Trp	Ile							
		210				215									

<210> 89

<211> 79

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Divergent  
subfamily of APPLE domains Consensus Sequence

<400> 89

Lys	Ser	Asp	Asp	Cys	Phe	Val	Arg	Leu	Pro	Asn	Thr	Lys	Leu	Pro	Asp
1				5					10					15	

Cura 468 SEQ list 0405.txt

Phe Ser Pro Ile Val Ile Ser Val Ala Ser Leu Glu Glu Cys Ala Gln  
20 25 30

Lys Cys Leu Asn Ser Asn Cys Ser Cys Arg Ser Phe Thr Tyr Asn Asn  
35 40 45

Asp Thr Lys Gly Cys Leu Leu Trp Ser Glu Ser Ser Leu Gly Asp Ala  
50 55 60

Arg Gln Leu Leu Pro Ser Gly Gly Val Asp Tyr Tyr Glu Lys Ile  
65 70 75

<210> 90

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Lipocalin/cytosolic fatty-acid binding protein  
family Consensus Sequence

<400> 90

Lys Phe Ala Gly Lys Trp Tyr Leu Val Ala Ser Ala Asn Phe Asp Pro  
1 5 10 15

Glu Leu Lys Glu Glu Leu Gly Val Leu Glu Ala Thr Arg Lys Glu Ile  
20 25 30

Thr Pro Leu Lys Glu Gly Asn Leu Glu Ile Val Phe Asp Gly Asp Lys  
35 40 45

Asn Gly Ile Cys Glu Glu Thr Phe Gly Lys Leu Glu Lys Thr Lys Lys  
50 55 60

Leu Gly Val Glu Phe Asp Tyr Tyr Thr Gly Asp Asn Arg Phe Val Val  
65 70 75 80

Leu Asp Thr Asp Tyr Asp Asn Tyr Leu Leu Val Cys Val Gln Lys Gly  
85 90 95

Asp Gly Asn Glu Thr Ser Arg Thr Ala Glu Leu Tyr Gly Arg Thr Pro  
100 105 110

Glu Leu Ser Pro Glu Ala Leu Glu Leu Phe Glu Thr Ala Thr Lys Glu  
115 120 125



Cura 468 SEQ list 0405.txt

Leu Gly Ile Pro Glu Asp Asn Val Val Cys Thr Arg Gln Thr Glu Arg  
 130 135 140

Cys  
 145

<210> 91  
 <211> 218  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Connexin  
 Consensus Sequence

<400> 91  
 Met Asp Trp Ser Phe Leu Gly Arg Leu Leu Glu Gly Val Asn Lys His  
 1 5 10 15  
 Ser Thr Ala Ile Gly Lys Ile Trp Leu Ser Val Leu Phe Ile Phe Arg  
 20 25 30  
 Ile Leu Val Leu Gly Val Ala Ala Glu Ser Val Trp Gly Asp Glu Gln  
 35 40 45  
 Ser Asp Phe Val Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val Cys  
 50 55 60  
 Tyr Asp Gln Phe Phe Pro Ile Ser His Val Arg Leu Trp Val Leu Gln  
 65 70 75 80  
 Leu Ile Phe Val Ser Thr Pro Ser Leu Leu Tyr Leu Gly His Val Ala  
 85 90 95  
 Tyr Arg Val Arg Arg Glu Glu Lys Leu Arg Glu Lys Glu Glu Glu His  
 100 105 110  
 Ser Lys Gly Leu Tyr Ser Glu Glu Ala Lys Lys Arg Cys Gly Ser Glu  
 115 120 125  
 Asp Gly Lys Val Arg Ile Arg Gly Gly Leu Trp Trp Thr Tyr Val Phe  
 130 135 140  
 Ser Ile Ile Phe Lys Ser Ile Phe Glu Val Gly Phe Leu Tyr Gly Gln  
 145 150 155 160

Cura 468 SEQ list 0405.txt

Tyr Leu Leu Tyr Gly Phe Thr Met Ser Pro Leu Val Val Cys Ser Arg  
165 170 175

Ala Pro Cys Pro His Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu  
180 185 190

Lys Thr Ile Phe Ile Val Phe Met Leu Val Val Ser Ala Ile Cys Leu  
195 200 205

Leu Leu Asn Leu Ala Glu Leu Phe Tyr Leu  
210 215

<210> 92

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Src homology 3  
domains Consensus Sequence

<400> 92

Glu Gly Pro Gln Val Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asp Pro  
1 5 10 15

Asp Glu Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys  
20 25 30

Ser Asp Asp Gly Trp Trp Lys Gly Arg Leu Gly Thr Gly Lys Glu Gly  
35 40 45

Leu Phe Pro Ser Asn Tyr Val Glu Glu Ile Asp  
50 55

<210> 93

<211> 57

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SH3 domain  
Consensus Sequence

<400> 93

Pro Lys Val Val Ala Leu Tyr Asp Tyr Gln Ala Arg Glu Ser Asp Glu  
1 5 10 15

Cura 468 SEQ list 0405.txt

Leu Ser Phe Lys Lys Gly Asp Ile Ile Ile Val Leu Glu Lys Ser Asp  
                   20                                  25                                  30

Asp Gly Gly Trp Trp Lys Gly Arg Leu Lys Gly Thr Lys Glu Gly Leu  
                   35                                  40                                  45

Ile Pro Ser Asn Tyr Val Glu Pro Val  
           50                                  55

<210> 94

<211> 91

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fes/CIP4  
           homology domain Consensus Sequence

<400> 94

Met Gly Phe Trp Ser Glu Leu Asp Asp Gly Phe Glu Ala Leu Leu Ser  
   1                                  5                                  10                                  15

Arg Leu Lys Asn Gly Leu Arg Leu Leu Glu Asp Leu Lys Lys Phe Met  
                   20                                  25                                  30

Arg Glu Arg Ala Lys Ile Glu Glu Glu Tyr Ala Lys Lys Leu Gln Lys  
                   35                                  40                                  45

Leu Ser Lys Lys Leu Arg Ala Val Arg Asp Thr Glu Ser Glu Leu Gly  
   50                                  55                                  60

Ser Leu Arg Lys Ala Trp Glu Val Leu Leu Ser Glu Thr Asp Ala Leu  
   65                                  70                                  75                                  80

Ala Lys Gln His Leu Gln Leu Ser Glu Asp Leu  
                                   85                                  90

<210> 95

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fes/CIP4  
           homology domain Consensus Sequence

Cura 468 SEQ list 0405.txt

<400> 95

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Met Gly Phe Gly Ser Glu Leu Cys Pro Glu Gly His Lys Ala Leu Leu
 1           5           10           15

Ser Arg Gln Asp Asn Glu Leu Arg Leu Leu Glu Glu Met Lys Lys Phe
           20           25           30

Met Ala Glu Arg Ala Lys Ile Glu Lys Glu Tyr Ala Gly Lys Leu Gln
           35           40           45

His Leu Ser Ala Gln Val Gly Lys Gly Pro Ala Thr Ala Glu Gly Glu
 50           55           60

Asp Glu Leu Ser Ser Leu Lys Ser Trp Ala Val Ile Leu Ser Glu Thr
 65           70           75           80

Glu Gln Gln Ser Lys Ile His Leu Gln Ile Ser Glu Asp Leu
           85           90

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<210> 96

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like  
serine protease Consensus Sequence

<400> 96

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Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
 1           5           10           15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
           20           25           30

Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
           35           40           45

Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
           50           55           60

Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
 65           70           75           80

Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
           85           90           95

```

Cura 468 SEQ list 0405.txt

Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro  
100 105 110

Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly  
115 120 125

Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln  
130 135 140

Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr  
145 150 155 160

Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu  
165 170 175

Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val  
180 185 190

Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser  
195 200 205

Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser  
210 215 220

Ser Tyr Leu Asp Trp Ile  
225 230

<210> 97

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin  
Consensus Sequence

<400> 97

Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val  
1 5 10 15

Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser  
20 25 30

Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser  
35 40 45

Cura 468 SEQ list 0405.txt

Val	Arg	Val	Val	Leu	Gly	Glu	His	Asn	Leu	Gly	Thr	Thr	Glu	Gly	Thr		
50						55					60						
Glu	Gln	Lys	Phe	Asp	Val	Lys	Lys	Ile	Ile	Val	His	Pro	Asn	Tyr	Asn		
65					70					75					80		
Pro	Asp	Thr	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Leu	Lys	Ser	Pro	Val	Thr		
				85					90					95			
Leu	Gly	Asp	Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro	Ser	Ala	Ser	Ser	Asp		
			100					105					110				
Leu	Pro	Val	Gly	Thr	Thr	Cys	Ser	Val	Ser	Gly	Trp	Gly	Arg	Thr	Lys		
		115					120					125					
Asn	Leu	Gly	Thr	Ser	Asp	Thr	Leu	Gln	Glu	Val	Val	Val	Pro	Ile	Val		
		130				135						140					
Ser	Arg	Glu	Thr	Cys	Arg	Ser	Ala	Tyr	Gly	Gly	Thr	Val	Thr	Asp	Thr		
145					150					155					160		
Met	Ile	Cys	Ala	Gly	Ala	Leu	Gly	Gly	Lys	Asp	Ala	Cys	Gln	Gly	Asp		
				165					170					175			
Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Asp	Gly	Glu	Leu	Val	Gly	Ile	Val		
			180					185					190				
Ser	Trp	Gly	Tyr	Gly	Cys	Ala	Val	Gly	Asn	Tyr	Pro	Gly	Val	Tyr	Thr		
		195					200					205					
Arg	Val	Ser	Arg	Tyr	Leu	Asp	Trp	Ile									
		210				215											

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NOV5 Primer 1

<400> 98

ctcccactcc tgctgcttct gact

24

<210> 99

Cura 468 SEQ list 0405.txt

<211> 25  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: NOV5 Primer 2  
  
<400> 99  
aaggctgggc ctaaccagc ctcac 25  
  
<210> 100  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: NOV7 Primer 1  
  
<400> 100  
catgaactgg gcatttctgc agg 23  
  
<210> 101  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: NOV7 Primer 2  
  
<400> 101  
ttatctgctg atctcgcagg ttatgga 27  
  
<210> 102  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: NOV8 Primer 1  
  
<400> 102  
ctgacaggcc ctggtgtgtg at 22

<210> 103  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV8 Primer 2

<400> 103  
tcacacatgt ttcatgtggg agttaga

27

<210> 104  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV9 Primer 1

<400> 104  
gagtgagagg tcggacagac tgtg

24

<210> 105  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV9 Primer 2

<400> 105  
actcatgcaa cttgcttctc tcactct

27

<210> 106  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: NOV10b Primer  
1

<400> 106  
cctatgagcc tgatgctgga tgac 24

<210> 107  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV10b Primer  
2

<400> 107  
aggactcaga ggagggagtc ctgag 25

<210> 108  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Forward

<400> 108  
gcactacaag tggaagcctt ac 22

<210> 109  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Probe

<400> 109  
ctcaagtaga agccgactta tgcaaa 26

Cura 468 SEQ list 0405.txt

<210> 110  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Reverse

<400> 110  
tcaaatcctt ctgcgataca gt 22

<210> 111  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b  
Forward

<400> 111  
cagctgcacg attaataag at 22

<210> 112  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b Probe

<400> 112  
aggtccttgga ctggccttca ccatt 25

<210> 113  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b  
Reverse

Cura 468 SEQ list 0405.txt

<400> 113  
ccaaagttgt gtccagactc at 22

<210> 114  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 114  
ccaaggaaga cctcttcatc tt 22

<210> 115  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 115  
tcttgcttac ggcataagcg ctctct 26

<210> 116  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 116  
ttcatttcta tgggacctca ga 22

<210> 117  
<211> 21  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Forward

<400> 117

aaagatggga ctcgtcatga c

21

<210> 118

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Probe

<400> 118

cacgccatct tactgactgg tctgga

26

<210> 119

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Reverse

<400> 119

gtgcaaattcc caaagtgtca

20

<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag4164 Forward

<400> 120

gcactacaag tggaagcctt ac

22

Cura 468 SEQ list 0405.txt

<210> 121  
<211> 26  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag4164 Probe

<400> 121  
ctcaagtaga agccgactta tgcaaa 26

<210> 122  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Reverse

<400> 122  
tcaaatacctt ctgcgataca gt 22

<210> 123  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 123  
ccaaggaaga cctcttcatc tt 22

<210> 124  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 124  
tcttgcttac ggcataagcg ctctct 26

<210> 125  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 125  
ttcatttcta tgggacctca ga 22

<210> 126  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 126  
ccaaggaaga cctcttcatc tt 22

<210> 127  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 127  
tcttgcttac ggcataagcg ctctct 26

<210> 128  
<211> 22  
<212> DNA  
<213> Artificial Sequence

Cura 468 SEQ list 0405.txt

<220>

<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 128

ttcatttcta tgggacctca ga

22

<210> 129

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Forward

<400> 129

aaagatggga ctcgtcatga c

21

<210> 130

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Probe

<400> 130

cacgccatct tactgactgg tctgga

26

<210> 131

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Reverse

<400> 131

gtgcaaattcc caaagtgtca

20

Cura 468 SEQ list 0405.txt

<210> 132  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b  
Forward

<400> 132  
cagctgcacg attaatagaag at 22

<210> 133  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b Probe

<400> 133  
aggctcttgga ctggccttca ccatt 25

<210> 134  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b  
Reverse

<400> 134  
ccaaagttgt gtccagactc at 22

<210> 135  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1537 Forward



Cura 468 SEQ list 0405.txt

<400> 135  
tttcaagaca ccctgtgata cc 22

<210> 136  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1537 Probe

<400> 136  
acttcgtgtc ctgaatgttc caggct 26

<210> 137  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1537 Reverse

<400> 137  
cagaggaatg aaggcataga tg 22

<210> 138  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2432 Forward

<400> 138  
gtaggcaaag ggactcactg t 21

<210> 139  
<211> 26  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2432 Probe

<400> 139

cagaaatcaa taatctttga ctgccg

26

<210> 140

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2432 Reverse

<400> 140

gcacattacg tggctgaga

19

<210> 141

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag1250 Forward

<400> 141

cgtggtgaac tctgccttat at

22

<210> 142

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag1250 Probe

<400> 142

cacagagctg tcgtctttga ccgatt

26

Cura 468 SEQ list 0405.txt

<210> 143  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1250 Reverse

<400> 143  
agtccctttg cctaccacaa t 21

<210> 144  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag3086 Forward

<400> 144  
ggacccatt cgactactgt 20

<210> 145  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag3086 Probe

<400> 145  
ctgatgacca gccgcatca atc 23

<210> 146  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag3086 Reverse

<400> 146  
ttctcaaact gcacctgggc 20

<210> 147  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag3797 Forward

<400> 147  
tctggacgac aactattgcc 20

<210> 148  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag3797 Probe

<400> 148  
atggtgctac actacggatc cgcag 25

<210> 149  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag3797 Reverse

<400> 149  
gtcacagaat tctcgctcga 20

<210> 150  
<211> 22  
<212> DNA  
<213> Artificial Sequence

Cura 468 SEQ list 0405.txt

<220>

<223> Description of Artificial Sequence: Ag2439 Forward

<400> 150

tatcatcact tgtgatggca aa

22

<210> 151

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2439 Probe

<400> 151

aaaaccgaga gcactttgaa aacaca

26

<210> 152

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2439 Reverse

<400> 152

aaacttctct cccagggtac aa

22

<210> 153

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2771 Forward

<400> 153

tgaacagaac tatgcgaaac aa

22

Cura 468 SEQ list 0405.txt

<210> 154  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Ag2771 Probe  
  
<400> 154  
tctgggtaag aagtactgcc ccaaacg 27  
  
<210> 155  
<211> 21  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Ag2771 Reverse  
  
<400> 155  
ggctcttcat ctttggaatga a 21  
  
<210> 156  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Ag1674 Forward  
  
<400> 156  
ctcactcacc acaaggagat aa 22  
  
<210> 157  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Ag1674 Probe  
  
<400> 157

tgacatcaaa ctcaacagtt cccagga

27

<210> 158

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag1674 Reverse

<400> 158

gtctaggaga gagctgagca aa

22

<210> 159

<211> 78

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PAN domain  
Consensus Sequence

<400> 159

Cys	Ser	Ser	Phe	Val	Arg	Val	Pro	Gly	Arg	Ser	Leu	Ser	Gly	Asn	Asp
1				5				10						15	

Ile	Ser	Val	Val	Asn	Val	Pro	Ser	Leu	Glu	Glu	Cys	Ala	Ala	Leu	Cys
			20					25					30		

Leu	Glu	Glu	Pro	Arg	Val	Cys	Arg	Ser	Phe	Thr	Tyr	Asn	Asn	Lys	Ser
		35					40					45			

Lys	Gln	Cys	Leu	Leu	Lys	Ser	Glu	Ser	Ser	Gly	Ser	Leu	Pro	Arg	Leu
	50					55					60				

Lys	Arg	Pro	Ser	Gln	Lys	Val	Asp	Tyr	Tyr	Glu	Lys	Ser	Cys
65					70					75			

<210> 160

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin  
homologues Consensus Sequence

<400> 160

Ser	Val	Trp	Gly	Asp	Glu	Gln	Ser	Asp	Phe	Thr	Cys	Asn	Thr	Gln	Gln
1				5				10					15		
Pro	Gly	Cys	Glu	Asn	Val	Cys	Tyr	Asp	Gln	Phe	Phe	Pro	Ile	Ser	His
			20					25					30		

Val Arg

<210> 161

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc Metalloprotease  
conserved domain

<400> 161

Asn Glu Gln Lys  
1

<210> 162

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc Metalloprotease  
conserved domain

<400> 162

Asn His Gln Lys  
1

<210> 163



<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc Metalloprotease conserved domain

<400> 163

Asn Asp Glu Gln

1

<210> 164

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc Metalloprotease conserved domain

<400> 164

Gln His Arg Lys

1

<210> 165

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc Metalloprotease conserved domain

<400> 165

Met Ile Leu Val

1

<210> 166

<211> 4

Cura 468 SEQ list 0405.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc Metalloprotease  
conserved domain

<400> 166

Met Ile Leu Phe

1